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RECOMBINANT TOXIN FRAGMENTS

This invention relates to recombinant toxin fragments, to DNA encoding these fragments and to their uses such as in a vaccine and for *in vitro* and *in vivo* purposes.

The clostridial neurotoxins are potent inhibitors of calcium-dependent neurotransmitter secretion in neuronal cells. They are currently considered to mediate this activity through a specific endoproteolytic cleavage of at least one of three vesicle or pre-synaptic membrane associated proteins VAMP, syntaxin or SNAP-25 which are central to the vesicle docking and membrane fusion events of neurotransmitter secretion. The neuronal cell targeting of tetanus and botulinum neurotoxins is considered to be a receptor mediated event following which the toxins become internalised and subsequently traffic to the appropriate intracellular compartment where they effect their endopeptidase activity.

The clostridial neurotoxins share a common architecture of a catalytic L-chain (LC, ca 50 kDa) disulphide linked to a receptor binding and translocating H-chain (HC, ca 100 kDa). The HC polypeptide is considered to comprise all or part of two distinct functional domains. The carboxy-terminal half of the HC (ca 50 kDa), termed the H_C domain, is involved in the high affinity, neurospecific binding of the neurotoxin to cell surface receptors on the target neuron, whilst the amino-terminal half, termed the H_N domain (ca 50 kDa), is considered to mediate the translocation of at least some portion of the neurotoxin across cellular membranes such that the functional activity of the LC is expressed within the target cell. The H_N domain also has the property, under conditions of low pH, of forming ion-permeable channels in lipid membranes, this may in some manner relate to its translocation function.

For botulinum neurotoxin type A (BoNT/A) these domains are considered to reside within amino acid residues 872-1296 for the H_C, amino acid residues 449-871 for the H_N and residues 1-448 for the LC. Digestion with trypsin effectively degrades the H_C domain of the BoNT/A to generate a non-toxic fragment designated LH_N, which is no longer able to bind to and enter neurons (Fig. 1). The LH_N fragment so produced also has the property

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of enhanced solubility compared to both the parent holotoxin and the isolated LC.

It is therefore possible to provide functional definitions of the domains within the neurotoxin molecule, as follows:

(A) clostridial neurotoxin light chain:

-a metalloprotease exhibiting high substrate specificity for vesicle and/or plasma - membrane associated proteins involved in the exocytotic process. In particular, it cleaves one or more of SNAP-25, VAMP (synaptobrevin / cellubrevin) and syntaxin.

(B) clostridial neurotoxin heavy chain H_N domain:

-a portion of the heavy chain which enables translocation of that portion of the neurotoxin molecule such that a functional expression of light chain activity occurs within a target cell.

-the domain responsible for translocation of the endopeptidase activity, following binding of neurotoxin to its specific cell surface receptor via the binding domain, into the target cell.

-the domain responsible for formation of ion-permeable pores in lipid membranes under conditions of low pH.

-the domain responsible for increasing the solubility of the entire polypeptide compared to the solubility of light chain alone.

(C) clostridial neurotoxin heavy chain H_C domain.

-a portion of the heavy chain which is responsible for binding of the native holotoxin to cell surface receptor(s) involved in the intoxicating action of clostridial toxin prior to internalisation of the toxin into the cell.

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The identity of the cellular recognition markers for these toxins is currently not understood and no specific receptor species have yet been identified although Kozaki et al. have reported that synaptotagmin may be the receptor for botulinum neurotoxin type B. It is probable that each of the neurotoxins has a different receptor.

It is desirable to have positive controls for toxin assays, to develop clostridial toxin vaccines and to develop therapeutic agents incorporating desirable properties of clostridial toxin.

However, due to its extreme toxicity, the handling of native toxin is hazardous.

The present invention seeks to overcome or at least ameliorate problems associated with production and handling of clostridial toxin.

Accordingly, the invention provides a polypeptide comprising first and second domains, wherein said first domain is adapted to cleave one or more vesicle or plasma-membrane associated proteins essential to neuronal exocytosis and wherein said second domain is adapted (i) to translocate the polypeptide into the cell or (ii) to increase the solubility of the polypeptide compared to the solubility of the first domain on its own or (iii) both to translocate the polypeptide into the cell and to increase the solubility of the polypeptide compared to the solubility of the first domain on its own, said polypeptide being free of clostridial neurotoxin and free of any clostridial neurotoxin precursor that can be converted into toxin by proteolytic action. Accordingly, the invention may thus provide a single polypeptide chain containing a domain equivalent to a clostridial toxin light chain and a domain providing the functional aspects of the H_N of a clostridial toxin heavy chain, whilst lacking the functional aspects of a clostridial toxin H_C domain.

In a preferred embodiment, the present invention provides a single chain polypeptide comprising first and second domains, wherein:-

said first domain is a clostridial neurotoxin light chain or a fragment or a variant thereof, wherein said first domain is capable of cleaving one or more vesicle or plasma

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membrane associated proteins essential to exocytosis; and

said second domain is a clostridial neurotoxin heavy chain H_N portion or a fragment or a variant thereof, wherein said second domain is capable of (i) translocating the polypeptide into a cell or (ii) increasing the solubility of the polypeptide compared to the solubility of the first domain on its own or (iii) both translocating the polypeptide into a cell and increasing the solubility of the polypeptide compared to the solubility of the first domain on its own; and wherein the second domain lacks a functional C-terminal part of a clostridial neurotoxin heavy chain designated H_C thereby rendering the polypeptide incapable of binding to cell surface receptors that are the natural cell surface receptors to which native clostridial neurotoxin binds.

In the above preferred embodiment, the first domain is qualified by a requirement for the presence of a particular cleavage function. Said cleavage function may be present when the light chain (L-chain) component is part of the single chain polypeptide molecule *per se*. Alternatively, the cleavage function may be substantially latent in the single chain polypeptide molecule, and may be activated by proteolytic cleavage of the single polypeptide between the first and second domains to form, for example, a dichain polypeptide molecule comprising the first and second domains disulphide bonded together.

The first domain is based on a clostridial neurotoxin light chain (L-chain), and embraces both fragments and variants of said L-chain so long as these components possess the requisite cleavage function. An example of a variant is an L-chain (or fragment thereof) in which one or more amino acid residues has been altered *vis-a-vis* a native clostridial L-chain sequence. In one embodiment, the modification may involve one or more conservative amino acid substitutions. Other modifications may include the removal or addition of one or more amino acid residues *vis-a-vis* a native clostridial L-chain sequence. However, any such fragment or variant must retain the aforementioned cleavage function.

The structure of clostridial neurotoxins was well known prior to the present invention -

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see, for example, Kurazono *et al* (1992) J. Biol. Chem., 267, 21, pp. 14721-14729. In particular, the Kurazono paper describes the minimum Domains required for cleavage activity (eg. proteolytic enzyme activity) of a clostridial neurotoxin L-chain. Similar discussion is provided by Poulain *et al* (1989) Eur. J. Biochem., 185, pp.197-203, by Zhou *et al* (1995), 34, pp.15175-15181, and by Blaustein *et al* (1987), 226, No.1, pp.115-120.

By way of exemplification, Table II on page 14726 of Kurazono *et al.* (1992) illustrates a number of L-chain deletion mutants (both amino-terminal and carboxy-terminal L-chain deletion mutants are illustrated). Such mutants, together with other L-chain mutants containing, for example, similar amino acid deletions or conservative amino acid substitutions are embraced by the first domain definition of the present invention provided that the L-chain component in question has the requisite cleavage activity.

Prior to the present application a number of conventional, simple assays were available to allow a skilled person to routinely confirm whether a given L-chain (or equivalent L-chain component) had the requisite cleavage activity. These assays are based on the inherent ability of a functional L-chain to effect peptide cleavage of specific vesicle or plasma membrane associated proteins (eg. synaptobrevin, syntaxin, or SNAP-25) involved in neuronal exocytosis, and simply test for the presence of the cleaved product/s of said proteolytic reaction.

For example, in a rough-and-ready assay, SNAP-25 (or synaptobrevin, or syntaxin) may be challenged with a test L-chain (or equivalent L-chain component), and then analysed by SDS-PAGE peptide separation techniques. Subsequent detection of peptides (eg. by silver staining) having molecular weights corresponding to the cleaved products of SNAP-25 (or other component of the neurosecretory machinery) would indicate the presence of an L-chain (or equivalent L-chain component) possessing the requisite cleavage activity.

In an alternative assay, SNAP-25 (or a different neuronal exocytosis molecule) may be challenged with a test L-chain (or equivalent L-chain component), and the cleavage

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products subjected to antibody detection as described in PCT/GB95/01279 (ie. WO95/33850) in the name of the present Applicant, Microbiological Research Authority. In more detail, a specific antibody is employed for detecting the cleavage of SNAP-25, which antibody recognises cleaved SNAP-25 but not uncleaved SNAP-25. Identification of the cleaved product by the antibody confirms the presence of an L-chain (or equivalent L-chain component) possessing the requisite cleavage activity. By way of exemplification, such a method is described in Examples 2 and 3 of PCT/GB96/00916 (ie. WO96/33273), also in the name of Microbiological Research Authority.

In a preferred embodiment of the present invention, the second domain is qualified by the ability to provide one or both of two functions, namely (i) translocation and/or (ii) increased solubility of the first domain.

The second domain is based on a H_N portion of a clostridial neurotoxin, which portion has been extensively described and characterised in the literature. Particular mention is made to Kurazono *et al* (1992) in which the structure of clostridial neurotoxin heavy chains is discussed together with the functions associated with the H_N and H_C portions thereof [see, for example, the bottom illustration in Fig. 1 on page 14722 of Kurazono *et al* (1992)]. In more detail, the H_N domain is a domain of a clostridial neurotoxin that functions to translocate a clostridial L-chain across the endosomal membrane of a vesicle, and is synonymous with the H₂ domain of a clostridial neurotoxin [see the bottom left-hand column and footer on page 197 of Poulain, B. *et al* (1989); see Fig. 1 in Blaustein, R. *et al* (1987); and see also the sentence bridging pages 178 and 179 of Shone, C. *et al* (1987), *Eur. J. Biochem.*, 167, pp. 175-180].

The second domain definition of the present invention includes fragments and variants of the H_N portion of a clostridial neurotoxin so long as these components provide the requisite (i) translocation and/or (ii) improved solubility function. An example of a variant is an H_N portion (or fragment thereof) in which one or more amino acid residues has been altered *vis-a-vis* a native clostridial H_N domain sequence. In one embodiment, the modification may involve one or more conservative amino acid substitutions. Other modifications may include the removal or addition of one or more amino acid residues

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vis-a-vis a native clostridial H_N sequence. However, any such fragment or variant must provide the aforementioned (i) translocation and/or (ii) improved solubility function.

The (i) translocation and (ii) improved solubility functions are now described in more detail.

Prior to the present application a number of conventional, simple assays were available to allow a skilled person to routinely confirm whether a particular clostridial neurotoxin H_N portion (or equivalent H_N component) had the requisite translocation function. In this respect, particular mention is made to the assays described in Shone *et al.* (1987) and Blaustein *et al.* (1987), which are now discussed.

These papers describe studies of the translocation function of clostridial neurotoxins, and demonstrate that the ability of said neurotoxins to form channels is associated with the presence of a translocation function.

Shone *et al.* (1987) describes an assay employing artificial liposomes loaded with potassium phosphate buffer (pH 7.2) and radiolabelled NAD. Thus, to confirm whether a test H_N portion (or equivalent H-chain component) of a clostridial neurotoxin has the requisite translocation function, the artificial liposomes are challenged with the test H_N portion. The release of K⁺ and NAD from the liposomes is indicative of a channel-forming activity, and thus the presence of a translocation function.

An alternative assay is described by Blaustein *et al.* (1987), wherein planar phospholipid bilayer membranes are used to test for channel-forming activity. Salt solutions on either side of the membrane are buffered at different pH - on the *cis* side, pH 4.7 or 5.5 and on the *trans* side, pH 7.4. Thus, to confirm whether a H_N portion (or equivalent H-chain component) of a clostridial neurotoxin has the requisite translocation function, the test H_N portion is added to the *cis* side of the membrane and electrical measurements made under voltage clamp conditions, in order to monitor the flow of current across the membrane (see paragraph 2.2 on pages 116-118). The presence of a desired translocation activity is confirmed by a steady rate of channel turn-on (see paragraph 3

on page 118).

Turning now to the second heavy chain function, namely (ii) increased solubility of the first domain. A conventional problem associated with the preparation of a clostridial neurotoxin L-chain molecules is that said L-chain molecules generally possess poor solubility characteristics. Thus, in one embodiment of the present invention, the fusion of a second domain (based on a H_N portion of a clostridial neurotoxin) to the L-chain increases the solubility of the L-chain. Similarly, the addition of a second domain to a L-chain equivalent molecule (eg. a fragment, or variant of a L-chain) increases the solubility of the L-chain equivalent molecule.

Prior to the present application a number of conventional, simple assays were available to allow a skilled person to routinely confirm whether a particular clostridial neurotoxin H_N portion (or equivalent H_N component) had the requisite ability to increase the solubility of a L-chain (or equivalent L-chain component). The most common method to assess solubility is through use of centrifugation, followed by a range of protein determination methods. For example, lysed *E. coli* cells containing expressed clostridial endopeptidase are centrifuged at 25,000 xg for 15 minutes to pellet cell debris and aggregated protein material. Following removal of the supernatant (containing soluble protein) the cell debris can be reconstituted in SDS-containing sample buffer (to solubilise the poorly soluble protein), prior to analysis of the two fractions by SDS-PAGE. Coomassie blue staining of electrophoresed protein, followed by densitometric analysis of the relevant protein band, facilitates a semi-quantitative analysis of solubility of expressed protein.

A further requirement of the single polypeptide molecule according to a preferred embodiment of the present invention is that the second domain lacks a functional C-terminal part of a clostridial neurotoxin heavy chain designated H_C , thereby rendering the polypeptide incapable of binding to cell surface receptors that are the natural cell surface receptors to which a native clostridial neurotoxin binds. This requirement is now discussed in more detail, and reference to incapable of binding throughout the present specification is to be interpreted as substantially incapable of binding, or reduced in

binding ability when compared with native clostridial neurotoxin.

It has been well documented, for example in the above-described literature and elsewhere, that native clostridial neurotoxin binds to specific target cells through a binding interaction that involves the H_C domain of the toxin heavy chain and a specific receptor on the target cell.

However, in contrast to native neurotoxin, the single polypeptide molecules according to a preferred embodiment of the present invention lack a functional H_C domain of native clostridial neurotoxin. Thus, the preferred single polypeptide molecules of the present invention are not capable of binding to the specific receptors targeted by native clostridial neurotoxin.

Prior to the present application a number of conventional, simple assays were available to allow a skilled person to routinely confirm whether a particular clostridial neurotoxin H_N portion (or equivalent H_N component) lacked the binding ability of native clostridial neurotoxin. In this respect, particular mention is made to the assays described by Shone *et al.* (1985) *Eur. J. Biochem.*, 151(1), pp. 75-82, and by Black & Dolly (1986) *J. Cell. Biol.*, 103, pp. 521-534. The basic Shone *et al.* (1985) method has been recently repeated in Sutton *et al.* (2001), 493, pp. 45-49 to assess the binding ability of tetanus toxins.

These papers describe simple methods for assessing binding of the H-chain of a clostridial neurotoxin to its target cells, motor neurons. Hence, these methods provide a means for routinely determining whether a modification to the H-chain results in a loss of or reduced native binding affinity of the H-chain for motor neurons. The methods are now discussed in more detail.

The Shone *et al.* (1985) method is based on a competitive binding assay in which test neurotoxin H-chain fragments are compared with radiolabelled native neurotoxin in their ability to bind to purified rat cerebrocortical synaptosomes (ie. native toxin target cells). A reduction of H_C function (ie. binding ability) is demonstrated by a reduced ability of the

test H-chain fragments to compete with the labelled intact toxin for binding to the synaptosomes (see page 76, column 1 to line 51-column 2, line 5).

Sutton *et al.* (2001) carried out similar competitive binding experiments using radiolabelled intact tetanus neurotoxin (TeNT) and unlabelled site-directed (TeNT) mutants. As above, a positive result in the assay is demonstrated by an inability of the mutant fragments to compete with the labelled TeNT for binding to synaptosomes.

An alternative approach is described by Black & Dolly (1986), which method employed electron microscopic autoradiography to visually assess binding of radiolabelled clostridial neurotoxins at the vertebrate neuromuscular junction, both *in vivo* and *in vitro*. Thus, this assay represents a simple visual method for confirming whether a test H_N domain (or equivalent H_N component) lacks a functional H_C domain.

There are numerous ways by which a second domain that lacks a functional H_C domain may be prepared. In this respect, inactivation of the H_C domain may be achieved at the amino acid level (eg. by use of a derivatising chemical, or a proteolytic enzyme), or at the nucleic acid level (eg. by use of site-directed mutagenesis, nucleotide/s insertion or deletion or modification, or by use of truncated nucleic acid).

For example, it would be routine for a skilled person to select a conventional derivatising chemical or proteolytic agent suitable for removal or modification of the H_C domain. Standard derivatising chemicals and proteolytic agents are readily available in the art, and it would be routine for a skilled person to confirm that said chemicals/agents provide an H_N domain with reduced or removed native binding affinity by following any one of a number of simple tests such as those described above.

Conventional derivatising chemicals may include any one of the following, which form a non-exhaustive list of examples:-

- (1) tyrosine derivatising chemicals such as anhydrides, more specifically maleic anhydride;

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- (2) diazonium based derivatising chemicals such as *bis*-Diazotized *o*-Tolidine, and diazotized *p*-aminobenzoyl biocytin;
- (3) EDC (1-ethyl 1-3-(3-dimethylaminopropyl) carbodiimide hydrochloride);
- (4) isocyanate based derivatising chemicals such as dual treatment with tetranitromethane followed by sodium dithionite; and
- (5) iodinating derivatising chemicals such as chloramine-T (N-chlorotoluene sulfonamide) or IODO-GEN (1,3,4,6-tetrachloro-3a,ba-diphenylglycouril).

Conventional proteolytic agents may include any one of the following, which form a non-exhaustive list of examples:-

- (1) trypsin [as demonstrated in Shone *et al* (1985)];
- (2) proline endopeptidase
- (3) lys C proteinase;
- (4) chymotrypsin;
- (5) thermolysin; and
- (6) arg C proteinase.

Alternatively, conventional nucleic acid mutagenesis methods may be employed to generate modified nucleic acid sequences that encode second domains lacking a functional H_C domain. For example, mutagenesis methods such as those described in Kurazono *et al* (1992) may be employed. A range of systems for mutagenesis of DNA are available, based on the DNA manipulation techniques described by:- Kunkel T. (1985) *Proc. Natl. Acad. Sci. USA*, 82, pp. 488-492; Taylor, J. W. *et al*. (1985) *Nucleic Acids Res.* 13, pp. 8749-8764 (1995); and Deng G. & Nickeloff J. A. (1992) *Anal. Biochem.*, 200, pp. 81-88.

According to all general aspects of the present invention, a polypeptide of the invention can be soluble but lack the translocation function of a native toxin-this is of use in providing an immunogen for vaccinating or assisting to vaccinate an individual against challenge by toxin. In a specific embodiment of the invention described in an example below a polypeptide designated LH₄₂₃/A elicited neutralising antibodies against type A

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neurotoxin. A polypeptide of the invention can likewise thus be relatively insoluble but retain the translocation function of a native toxin - this is of use if solubility is imparted to a composition made up of that polypeptide and one or more other components by one or more of said other components.

The first domain of the polypeptide of the invention cleaves one or more vesicle or plasma-membrane associated proteins essential to the specific cellular process of exocytosis, and cleavage of these proteins results in inhibition of exocytosis, typically in a non-cytotoxic manner. The cell or cells affected are not restricted to a particular type or subgroup but can include both neuronal and non-neuronal cells. The activity of clostridial neurotoxins in inhibiting exocytosis has, indeed, been observed almost universally in eukaryotic cells expressing a relevant cell surface receptor, including such diverse cells as from *Aplysia* (sea slug), *Drosophila* (fruit fly) and mammalian nerve cells, and the activity of the first domain is to be understood as including a corresponding range of cells.

The polypeptide of the invention may be obtained by expression of a recombinant nucleic acid, preferably a DNA, and is a single polypeptide, that is to say not cleaved into separate light and heavy chain domains. The polypeptide is thus available in convenient and large quantities using recombinant techniques.

In a polypeptide according to the invention, said first domain preferably comprises a clostridial toxin light chain or a fragment or variant of a clostridial toxin light chain. The fragment is optionally an N-terminal, or C-terminal fragment of the light chain, or is an internal fragment, so long as it substantially retains the ability to cleave the vesicle or plasma-membrane associated protein essential to exocytosis. The minimal domains necessary for the activity of the light chain of clostridial toxins are described in *J. Biol. Chem.*, Vol.267, No. 21, July 1992, pages 14721-14729. The variant has a different peptide sequence from the light chain or from the fragment, though it too is capable of cleaving the vesicle or plasma-membrane associated protein. It is conveniently obtained by insertion, deletion and/or substitution of a light chain or fragment thereof. In embodiments of the invention described below a variant sequence comprises (i) an N-terminal extension to a clostridial toxin light chain or fragment (ii) a clostridial toxin light

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chain or fragment modified by alteration of at least one amino acid (iii) a C-terminal extension to a clostridial toxin light chain or fragment, or (iv) combinations of 2 or more of (i)-(iii).

The first domain preferably exhibits endopeptidase activity specific for a substrate selected from one or more of SNAP-25, synaptobrevin/VAMP and syntaxin. The clostridial toxin is preferably botulinum toxin or tetanus toxin.

In one embodiment of the invention described in an example below, the toxin light chain and the portion of the toxin heavy chain are of botulinum toxin type A. In a further embodiment of the invention described in an example below, the toxin light chain and the portion of the toxin heavy chain are of botulinum toxin type B. The polypeptide optionally comprises a light chain or fragment or variant of one toxin type and a heavy chain or fragment or variant of another toxin type.

In a polypeptide according to the invention said second domain preferably comprises a clostridial toxin heavy chain H_N portion or a fragment or variant of a clostridial toxin heavy chain H_N portion. The fragment is optionally an N-terminal or C-terminal or internal fragment, so long as it retains the function of the H_N domain. Teachings of regions within the H_N responsible for its function are provided for example in Biochemistry 1995, 34, pages 15175-15181 and Eur. J. Biochem, 1989, 185, pages 197-203. The variant has a different sequence from the H_N domain or fragment, though it too retains the function of the H_N domain. It is conveniently obtained by insertion, deletion and/or substitution of a H_N domain or fragment thereof. In embodiments of the invention, described below, it comprises (i) an N-terminal extension to a H_N domain or fragment, (ii) a C-terminal extension to a H_N domain or fragment, (iii) a modification to a H_N domain or fragment by alteration of at least one amino acid, or (iv) combinations of 2 or more of (i)-(iii). The clostridial toxin is preferably botulinum toxin or tetanus toxin.

The invention also provides a polypeptide comprising a clostridial neurotoxin light chain and a N-terminal fragment of a clostridial neurotoxin heavy chain, the fragment preferably comprising at least 423 of the N-terminal amino acids of the heavy chain of botulinum

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toxin type A, 417 of the N-terminal amino acids of the heavy chain of botulinum toxin type B or the equivalent number of N-terminal amino acids of the heavy chain of other types of clostridial toxin such that the fragment possesses an equivalent alignment of homologous amino acid residues.

These polypeptides of the invention are thus not composed of two or more polypeptides, linked for example by di-sulphide bridges into composite molecules. Instead, these polypeptides are single chains and are not active or their activity is significantly reduced in an *in vitro* assay of neurotoxin endopeptidase activity.

Further, the polypeptides may be susceptible to be converted into a form exhibiting endopeptidase activity by the action of a proteolytic agent, such as trypsin. In this way it is possible to control the endopeptidase activity of the toxin light chain.

In further embodiments of the invention, the polypeptide contains an amino acid sequence modified so that (a) there is no protease sensitive region between the LC and H_N components of the polypeptide, or (b) the protease sensitive region is specific for a particular protease. This latter embodiment is of use if it is desired to activate the endopeptidase activity of the light chain in a particular environment or cell. Though, in general, the polypeptides of the invention are activated prior to administration.

More generally, a proteolytic cleavage site may be introduced between any two domains of the single chain polypeptide molecule.

For example, a cleavage site may be introduced between the first and second domains such that cleavage thereof converts the single chain polypeptide molecule into a dichain polypeptide structure wherein the first and second domains are linked together by a disulphide bond. Specific Examples of such molecules are provided by SEQ IDs 11-18 of the present application in which an Factor Xa cleavage site has been introduced between the first domain (L-chain) and the second domain (H_N).

A range of peptide sequences having inherent cleavage sites are available for insertion

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into the junction between one or more domains of a polypeptide according to the present invention. For example, insertion of a cleavage site between the first (L-chain) and second (H_N) domains may result in a single polypeptide chain molecule that is proteolytically cleavable to form a dichain polypeptide in which the first and second domains are held together by a disulphide bond between the first and second domains. The proteolytic cleavage may be performed *in vitro* prior to use, or *in vivo* by cell specific activation through intracellular proteolytic action.

Alternatively (or additionally), a cleavage site may be introduced between the second and third domains, or between the purification tag and the polypeptide of the present invention. The third domain and purification tag aspects of the present invention are discussed in more detail below.

To facilitate convenient insertion of a range of cleavage sites into the junction between the LC and H_N domains, it is preferable to prepare an expression clone that can serve as a template for future clone development. Such a template is represented by SEQ ID 103, in which the DNA encoding LH_N/B has been modified by standard mutagenesis techniques to incorporate unique restriction enzyme sites. To incorporate new cleavage sites at the junction requires simple insertion of novel oligonucleotides encoding the new cleavage site.

Suitable cleavage sites include, but are not limited to, those described in Table 1.

Table 1 - Cleavage site (eg. between the first and second domains for LH_N activation)

<u>Protease</u>	<u>Amino acid sequence of recognition site</u>	<u>SEQ ID exemplification</u>
Factor Xa	I-E/D-G-R ↓	71/72, 33/34, 55/56, 57/58, 115/116, 117/118, 119/120, 121/122
Enterokinase	D-D-D-D-K ↓	69/70, 31/32, 29/30,

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		43/44, 45/46, 113/114, 111/112, 59/60, 61/62, 63/64, 65/66, 79/80, 81/82, 83-98, 105/106, 107/108
Precission	L-E-V-L-F-Q ↓↓ G-P	75/76, 35/36, 51/52, 53/54
Thrombin	L-V-P-R ↓↓ G-S	77/78, 37/38, 47/48, 49/50, 99/100
Genenase	H-Y ↓↓ or Y ↓↓ -H	
TEV	E-N-L-Y-F-Q ↓↓ G	101/102
Furin	R-X-X-R ↓↓, preferred R-X-K/R-R ↓↓	

(wherein X = any amino acid)

In some cases, the use of certain cleavage sites and corresponding proteolytic enzymes (eg. precission, thrombin) will leave a short N-terminal extension on the polypeptide at a position C-terminal to the cleavage site (see the ↓↓ cleavage pattern for the exemplified proteases in Table 1).

Peptide sequences may be introduced between any two domains to facilitate specific cleavage of the domains at a later stage. This approach is commonly used in proprietary expression systems for cleavage and release of a purification tag (eg. maltose-binding protein (MBP), glutathione S-transferase (GST), polyhistidine tract (His6)) from a fusion protein that includes the purification tag. In this respect, the purification tag is preferably fused to the N- or C-terminus of the polypeptide in question.

The choice of cleavage site may have a bearing on the precise nature of the N-terminus (or C-terminus) of the released polypeptide. To illustrate this, identical LH_N/B fragments produced in such proprietary systems are described in SEQ ID 88, 94, 96, 98, in which the N-terminal extensions to the LH_N/B sequence are ISEFGS, GS, SPGARGS &

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AMADIGS respectively. In the case of LH_N/C fragments, SEQ ID 126, 128 & 130 describe the N-terminal sequences VPEFGSSRV_NDH, ISEFGSSRV_NDH and VPEFGSSRV_NDH following release of the LH_N/C fragment from its fusion tag by enterokinase, genenase and Factor Xa respectively. Each of these extension peptide sequences is an example of a variant L-chain sequence of the present invention. Similarly, if the purification tag were to be fused to the C-terminal end of the second domain, the resulting cleaved polypeptide (ie. fusion protein minus purification tag) would include C-terminal extension amino acids. Each of these extension peptides provides an example of a variant H_N-portion of the present invention.

In some cases, cleavage at a specific site, for example, between a purification tag and a polypeptide of the present invention may be of lower efficiency than desired. To address this potential problem, the present Applicant has modified proprietary vectors in two particular ways, which modifications may be employed individually or in combination with each other. Whilst said modifications may be applied to cleavage sites between any two domains in a polypeptide or fusion protein according to the present invention, the following discussion simply illustrates a purification tag-first domain cleavage event.

First, the DNA is modified to include an additional peptide spacer sequence, which optionally may represent one or more additional cleavage sites, at the junction of the purification tag and the polypeptide. Examples of the full-length expressed polypeptide from this approach are presented in SEQ ID 86, 90 & 92. Such an approach has resulted in efficient cleavage and release of the polypeptide of interest. Depending on the presence and nature of any intra-polypeptide cleavage sites (eg. between the first and second domains), cleavage of the purification tag from the fusion protein may occur simultaneously to proteolytic cleavage between the first and second domains. Alternatively, release of the purification tag may occur without proteolytic cleavage between the first and second domains. These two cleavage schemes are illustrated in Figure 14.

Depending on the cleavage enzyme chosen, this strategy may result in a short amino acid extension to the N-terminus (or C-terminus) of the polypeptide. For example, in the

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case of SEQ ID 92, cleavage of the expressed product with enterokinase results in two polypeptides coupled by a single disulphide bond at the first domain-second domain junction (ie. the L chain-H_N junction), with a short N-terminal peptide extension that resembles an intact Factor Xa site and a short N-terminal extension due to polylinker sequence (IEGRISEFGS).

Secondly, the DNA encoding a self-splicing intein sequence may be employed, which intein may be induced to self-splice under pH and/or temperature control. The intein sequence (represented in SEQ ID 110 as the polypeptide sequence ISEFRESGAISGDSLISLASTGKRVS IKDLLDEKDFEIWAINEQTMKLESAKVS RVFCTG KKLVIYILKTRLGRTIKATANHRFLTIDGWKRLDELSLKEHIALPRKLESSSLQLSPEIEKL SQSDIYWDSIVSITETGV EEVFDLTVPGPHNFVANDIIVHN) facilitates self-cleavage of the illustrated polypeptide (ie. purification tag-LH_N/B) to yield a single polypeptide molecule with no purification tag. This process does not therefore require treatment of the initial expression product with proteases, and the resultant polypeptide (ie. L-chain - Factor Xa activation site - H_N) is simply illustrative of how this approach may be applied.

According to a further embodiment of the invention, which is described in an example below, there is provided a polypeptide lacking a portion designated H_C of a clostridial toxin heavy chain. This portion, seen in the naturally produced toxin, is responsible for binding of toxin to cell surface receptors prior to internalisation of the toxin. This specific embodiment is therefore adapted so that it can not be converted into active toxin, for example by the action of a proteolytic enzyme. The invention thus also provides a polypeptide comprising a clostridial toxin light chain and a fragment of a clostridial toxin heavy chain, said fragment being not capable of binding to those cell surface receptors involved in the intoxicating action of clostridial toxin, and it is preferred that such a polypeptide lacks an intact portion designated H_C of a clostridial toxin heavy chain.

In further embodiments of the invention there are provided compositions containing a polypeptide comprising a clostridial toxin light chain and a portion designated H_N of a clostridial toxin heavy chain, and wherein the composition is free of clostridial toxin and free of any clostridial toxin precursor that may be converted into clostridial toxin by the

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action of a proteolytic enzyme. Examples of these compositions include those containing toxin light chain and H_N sequences of botulinum toxin types A, B, C₁, D, E, F and G.

The polypeptides of the invention are conveniently adapted to bind to, or include, a third domain (eg. a ligand for targeting to desired cells). The polypeptide optionally comprises a sequence that binds to, for example, an immunoglobulin. A suitable sequence is a tandem repeat synthetic IgG binding domain derived from domain B of Staphylococcal protein A. Choice of immunoglobulin specificity then determines the target for a polypeptide-immunoglobulin complex. Alternatively, the polypeptide comprises a non-clostridial sequence that binds to a cell surface receptor, suitable sequences including insulin-like growth factor-1 (IGF-1) which binds to its specific receptor on particular cell types and the 14 amino acid residue sequence from the carboxy-terminus of cholera toxin A subunit which is able to bind the cholera toxin B subunit and thence to GM1 gangliosides. A polypeptide according to the invention thus, optionally, further comprises a third domain adapted for binding of the polypeptide to a cell.

In a preferred embodiment, the third domain binds to a receptor on a target cell, which receptor is susceptible to endosomal processing.

According to a second aspect the invention there is provided a fusion protein comprising a fusion of (a) a polypeptide of the invention as described above with (b) a second polypeptide (also known as a purification tag) adapted for binding to a chromatography matrix so as to enable purification of the fusion protein using said chromatography matrix. It is convenient for the second polypeptide to be adapted to bind to an affinity matrix, such as a glutathione Sepharose, enabling rapid separation and purification of the fusion protein from an impure source, such as a cell extract or supernatant.

One possible second purification polypeptide is glutathione-S-transferase (GST), and others will be apparent to a person of skill in the art, being chosen so as to enable purification on a chromatography column according to conventional techniques.

According to another embodiment of the present invention, spacer sequences may be

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introduced between two or more domains of the single chain polypeptide molecule. For example, a spacer sequence may be introduced between the second and third domains of a polypeptide molecule of the present invention. Alternatively (or in addition), a spacer sequence may be introduced between a purification tag and the polypeptide of the present invention or between the first and second domains. A spacer sequence may include a proteolytic cleavage site.

In more detail, insertion of a specific peptide sequence into the second domain-third domain junction may be performed with the purpose of spacing the third domain (eg. ligand) from the second domain (eg. H_N). This approach may facilitate efficient interaction of the third domain with the specific binding target and/or improve the folding characteristics of the polypeptide. Example spacer peptides are provided in Table 2.

Table 2 - spacer sequences

<u>Sequence</u>	<u>Illustrated in SEQ ID No</u>
(GGGGS) ₃	39/40, 43/44, 49/50, 53/54, 57/58
RNAse A loop	138/139
Helical	41/42, 45/46, 47/48, 51/52, 55/56
Att sites (TSLYKKAGFGS or DPAFLYKV)	133

In a preferred embodiment, a spacer sequence may be introduced between the first and second domains. For example, a variety of first domain (eg. L-chain) expression constructs have been prepared that incorporate features that are advantageous to the preparation of novel single polypeptide hybrid first domain-second domain fusions. Such expression cassettes are illustrated by SEQ ID NO 69, 71, 73, 75, 77 & 113.

The above cassettes take advantage of a natural linker sequence that exists in the region between the C-terminus of the L-chain and the N-terminus of the H_N domain of a native clostridial neurotoxin. In more detail, there is a cysteine at each end of the natural linker sequence that serve to couple the L-chain and H_N domain together following proteolytic cleavage of the single chain polypeptide molecule into its dichain counterpart. These cysteine groups are preserved in the above-mentioned cassettes.

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Thus, by maintaining the cysteine amino acids at either end of the linker sequence, and optionally incorporating a specific proteolytic site to replace the native sequence, a variety of constructs have been prepared that have the property of being specifically cleavable between the first and second domains.

For example, by fusing a sequence of interest, such as H_N/B to the sequence described in SEQ ID 69, it is possible to routinely prepare L-chain/A- H_N/B novel hybrids that are linked through a specific linker region that facilitates disulphide bond formation. Thus, the expressed fusion proteins are suitable for proteolytic cleavage between the first (L-chain) and second (H_N) domains. The same linkers, optionally including said cleavage site, may be used to link together other domains of the polypeptide or fusion protein of the present invention.

In a further embodiment of the present invention, molecular clamps may be used to clamp together two or more domains of the polypeptides or fusion proteins of the present invention. Molecular clamps may be considered a particular sub-set of the aforementioned spacer sequences.

In more detail, molecular clamping (also known as directed coupling) is a method for joining together two or more polypeptide domains through the use of specific complementary peptide sequences that facilitate non-covalent protein-protein interactions.

Examples of such peptide sequences include leucine zippers (jun & fos), polyionic peptides (eg. poly-glutamate and its poly-arginine pair) and the synthetic IgG binding domain of Staphylococcal protein A.

Polypeptides comprising first and second domains (eg. LH_N) have been prepared with molecular clamping sequences fused to the C-terminus of the second (eg. H_N) domain through two methods.

First, DNA encoding the molecular clamp has been ligated directly to the DNA encoding

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an LH_N polypeptide, after removing the STOP codon present in the LH_N coding sequence. By insertion, to the 3' of the LH_N sequence, of overlapping oligonucleotides encoding the clamp sequence and a 3' STOP codon, an expression cassette has been generated. An example of such a sequence is presented in SEQ ID 63 in which the DNA sequence coding for the molecular clamp known as fos (LTDTLQAETDQLEDEKSAIQTEIANLLKEKEKLEFILAHH) has been introduced to the 3' of a nucleic acid molecule encoding a LH_N/A polypeptide, which molecule also has a nucleic acid sequence encoding an enterokinase cleavage site between the coding regions of the first domain (L-chain) and the second domain (H_N).

Secondly, site-specific recombination has been utilised to incorporate a clamp sequence to the 3' of a LH_N polypeptide (see, for example, the GATEWAY system described below) spaced from the H_N domain by the short peptide Gly-Gly. Use of this peptide to space clamp sequences from the C-terminus of H_N is illustrated in SEQ 117/118.

In some embodiments, it may be preferable to incorporate cysteine side chains into the clamp peptide to facilitate formation of disulphide bonds across the clamp, and so make a covalent linkage between the, for example, second domain (H_N) and a third domain (eg. a ligand). Incorporation of the cysteine codon into the clamp sequence has been performed by standard techniques, to result in sequences of the type represented by SEQ ID 59/60, 61/62, 117/118 and 119/120.

A schematic for the application of molecular clamping to the preparation of suitable LH_N polypeptides is illustrated in Figure 15.

A further alternative for expression of a full-length polypeptide containing first and second domains that is suitable for site-specific coupling to a third domain (eg. a ligand) is to incorporate an intein self-cleaving sequence into the 3' of the second domain (eg. H_N). SEQ ID 67/68 illustrates one such construct, in which LH_N/A having an enterokinase cleavage site between the first (eg. L-chain) and second (eg. H_N) domains is expressed with a Cys residue at the C-terminus, followed by the intein sequence.

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Following self-cleavage, a reactive thioester is then formed that can take part in a directed coupling reaction to a third domain, for example, as described by Bruick *et al*, Chem. Biol. (1996), pp. 49-56. Such a polypeptide facilitates site-specific chemical coupling to third domains (eg. ligands of interest) without the problems associated with random derivatisation and random coupling which may otherwise result in a heterogenous final product.

As will be appreciated by a skilled person from the entire disclosure of the present application, first and second domains may employ L-chain and H-chain components from any clostridial neurotoxin source. Whilst botulinum sources may be preferred, tetanus sources have equal applicability. In this respect, the whole sequence of tetanus neurotoxin (TeNT) as published prior to the present application by Eisel, U. *et al* (1986) EMBO J. 5 (10), pp. 2495-2502, and Accession No. X04436 is included in the present application as SEQ ID 140/141 for ease of reference.

To help illustrate this point, several TeNT based polypeptides have been prepared according to the present invention, and reference is made to SEQ ID 143 which is an LH_N polypeptide having a C-terminal sequence of EEDIDV₈₇₉. Reference is also made to SEQ ID 147 which is an LH_N polypeptide having a C-terminal sequence of EEDIDVILKKSTIL₈₈₇. Both of these LH_N sequences are representative of 'native' TeNT LH_N sequences, which have no introduced specific cleavage site between the L-chain and the H_N domain. Thus, SEQ ID 145 illustrates a TeNT polypeptide according to the present invention in which the natural TeNT linker region between the L-chain and the H_N domain has been replaced with a polypeptide containing a specific enterokinase cleavage sequence.

It will be also appreciated that the general approaches described in the present specification for introducing specific cleavage sites and spacer/clamping sequences between any two domains (eg. the L-chain and the H_N domain, or the L-chain and a purification tag) are routinely applicable to the preparation of TeNT-containing polypeptide molecules according to the present invention.

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A third aspect of the invention provides a composition comprising a derivative of a clostridial toxin, said derivative retaining at least 10% of the endopeptidase activity of the clostridial toxin, said derivative further being non-toxic *in vivo* due to its inability to bind to cell surface receptors, and wherein the composition is free of any component, such as toxin or a further toxin derivative, that is toxic *in vivo*. The activity of the derivative preferably approaches that of natural toxin, and is thus preferably at least 30% and most preferably at least 60% of natural toxin. The overall endopeptidase activity of the composition will, of course, also be determined by the amount of the derivative that is present.

While it is known to treat naturally produced clostridial toxin to remove the H_C domain, this treatment does not totally remove toxicity of the preparation, instead some residual toxin activity remains. Natural toxin treated in this way is therefore still not entirely safe. The composition of the invention, derived by treatment of a pure source of polypeptide advantageously is free of toxicity, and can conveniently be used as a positive control in a toxin assay, as a vaccine against clostridial toxin or for other purposes where it is essential that there is no residual toxicity in the composition.

The invention enables production of the polypeptides and fusion proteins of the invention by recombinant means.

A fourth aspect of the invention provides a nucleic acid encoding a polypeptide or a fusion protein according to any of the aspects of the invention described above.

In one embodiment of this aspect of the invention, a DNA sequence provided to code for the polypeptide or fusion protein is not derived from native clostridial sequences, but is an artificially derived sequence not preexisting in nature.

A specific DNA (SEQ ID NO: 1) described in more detail below encodes a polypeptide or a fusion protein comprising nucleotides encoding residues 1-871 of a botulinum toxin type A. Said polypeptide comprises the light chain domain and the first 423 amino acid residues of the amino terminal portion of a botulinum toxin type A heavy chain. This

recombinant product is designated LH₄₂₃/A (SEQ ID NO: 2).

In a second embodiment of this aspect of the invention a DNA sequence which codes for the polypeptide or fusion protein is derived from native clostridial sequences but codes for a polypeptide or fusion protein not found in nature.

A specific DNA (SEQ ID NO: 19) described in more detail below encodes a polypeptide or a fusion protein and comprises nucleotides encoding residues 1-1171 of a botulinum toxin type B. Said polypeptide comprises the light chain domain and the first 728 amino acid residues of the amino terminal protein of a botulinum type B heavy chain. This recombinant product is designated LH₇₂₈/B (SEQ ID NO: 20).

The invention thus also provides a method of manufacture of a polypeptide comprising expressing in a host cell a DNA according to the third aspect of the invention. The host cell is suitably not able to cleave a polypeptide or fusion protein of the invention so as to separate light and heavy toxin chains; for example, a non-clostridial host.

The invention further provides a method of manufacture of a polypeptide comprising expressing in a host cell a DNA encoding a fusion protein as described above, purifying the fusion protein by elution through a chromatography column adapted to retain the fusion protein, eluting through said chromatography column a ligand adapted to displace the fusion protein and recovering the fusion protein. Production of substantially pure fusion protein is thus made possible. Likewise, the fusion protein is readily cleaved to yield a polypeptide of the invention, again in substantially pure form, as the second polypeptide may conveniently be removed using the same type of chromatography column.

The LH_N/A derived from dichain native toxin requires extended digestion with trypsin to remove the C-terminal 1/2 of the heavy chain, the H_C domain. The loss of this domain effectively renders the toxin inactive *in vivo* by preventing its interaction with host target cells. There is, however, a residual toxic activity which may indicate a contaminating, trypsin insensitive, form of the whole type A neurotoxin.

In contrast, the recombinant preparations of the invention are the product of a discreet, defined gene coding sequence and can not be contaminated by full length toxin protein. Furthermore, the product as recovered from *E. coli*, and from other recombinant expression hosts, is an inactive single chain peptide or if expression hosts produce a processed, active polypeptide it is not a toxin. Endopeptidase activity of LH₄₂₃/A, as assessed by the current *in vitro* peptide cleavage assay, is wholly dependent on activation of the recombinant molecule between residues 430 and 454 by trypsin. Other proteolytic enzymes that cleave between these two residues are generally also suitable for activation of the recombinant molecule. Trypsin cleaves the peptide bond C-terminal to Arginine or C-terminal to Lysine and is suitable as these residues are found in the 430-454 region and are exposed (see Fig. 12).

The recombinant polypeptides of the invention are potential therapeutic agents for targeting to cells expressing the relevant substrate but which are not implicated in effecting botulism. An example might be where secretion of neurotransmitter is inappropriate or undesirable or alternatively where a neuronal cell is hyperactive in terms of regulated secretion of substances other than neurotransmitter. In such an example the function of the H_C domain of the native toxin could be replaced by an alternative targeting sequence providing, for example, a cell receptor ligand and/or translocation domain.

One application of the recombinant polypeptides of the invention will be as a reagent component for synthesis of therapeutic molecules, such as disclosed in WO-A-94/21300.

The recombinant product will also find application as a non-toxic standard for the assessment and development of *in vitro* assays for detection of functional botulinum or tetanus neurotoxins either in foodstuffs or in environmental samples, for example as disclosed in EP-A-0763131.

A further option is addition, to the C-terminal end of a polypeptide of the invention, of a peptide sequence which allows specific chemical conjugation to targeting ligands of both protein and non-protein origin.

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In yet a further embodiment an alternative targeting ligand is added to the N-terminus of polypeptides of the invention. Recombinant LH_N derivatives have been designated that have specific protease cleavage sites engineered at the C-terminus of the LC at the putative trypsin sensitive region and also at the extreme C-terminus of the complete protein product. These sites will enhance the activational specificity of the recombinant product such that the dichain species can only be activated by proteolytic cleavage of a more predictable nature than use of trypsin.

The LH_N enzymatically produced from native BoNT/A is an efficient immunogen and thus the recombinant form with its total divorce from any full length neurotoxin represents a vaccine component. The recombinant product may serve as a basal reagent for creating defined protein modifications in support of any of the above areas.

Recombinant constructs are assigned distinguishing names on the basis of their amino acid sequence length and their Light Chain (L-chain, L) and Heavy Chain (H-chain, H) content as these relate to translated DNA sequences in the public domain or specifically to SEQ ID NO: 2 and SEQ ID NO: 20. The 'LH' designation is followed by '/X' where 'X' denotes the corresponding clostridial toxin serotype or class, e.g. 'A' for botulinum neurotoxin type A or 'TeTx' for tetanus toxin. Sequence variants from that of the native toxin polypeptide are given in parenthesis in standard format, namely the residue position number prefixed by the residue of the native sequence and suffixed by the residue of the variant:

Subscript number prefixes indicate an amino-terminal (N-terminal) extension, or where negative a deletion, to the translated sequence. Similarly, subscript number suffixes indicate a carboxy terminal (C-terminal) extension or where negative numbers are used, a deletion. Specific sequence inserts such as protease cleavage sites are indicated using abbreviations, e.g. Factor Xa is abbreviated to FXa. L-chain C-terminal suffixes and H-chain N-terminal prefixes are separated by a '/' to indicate the predicted junction between the L and H-chains. Abbreviations for engineered ligand sequences are prefixed or suffixed to the clostridial L-chain or H-chain corresponding to their position in the translation product.

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Following this nomenclature,

- LH₄₂₃/A = SEQ ID NO: 2, containing the entire L-chain and 423 amino acids of the H-chain of botulinum neurotoxin type A;
- ₂LH₄₂₃/A = a variant of this molecule, containing a two amino acid extension to the N-terminus of the L-chain;
- ₂L₂H₄₂₃/A = a further variant in which the molecule contains a two amino acid extension on the N-terminus of both the L-chain and the H-chain;
- ₂L_{FXa/2}H₄₂₃/A = a further variant containing a two amino acid extension to the N-terminus of the L-chain, and a Factor Xa cleavage sequence at the C-terminus of the L-chain which, after cleavage of the molecule with Factor Xa leaves a two amino acid N-terminal extension to the H-chain component; and
- ₂L_{FXa/2}H₄₂₃/A-IGF-1 = a variant of this molecule which has a further C-terminal extension to the H-chain, in this example the insulin-like growth factor 1 (IGF-1) sequence.

The basic molecular biology techniques required to carry out the present invention were readily available in the art before the priority date of the present application and, as such, would be routine to a skilled person.

Example 1 of the present application illustrates conventional restriction endonuclease-dependent cleavage and ligation methodologies for preparing nucleic acid sequences encoding polypeptides of the present invention.

Example 4 *et seq* illustrate a number of alternative conventional methods for

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engineering recombinant DNA molecules that do not require traditional methods of restriction endonuclease-dependent cleavage and ligation of DNA. One such method is the site-specific recombination GATEWAY (trade mark) cloning system of Invitrogen, Inc., which uses phage lambda-based site-specific recombination [Landy, A. (1989) Ann. Rev. Biochem. 58, pp. 913-949]. This method is now described in slightly more detail.

Using standard restriction endonuclease digestion, or polymerase chain reaction techniques, a DNA sequence encoding first and second domains (eg. a BoNT LH_N molecule) may be cloned into an Entry Vector. There are a number of options for creation of the correct coding region flanked by requisite *att* site recombination sequences, as described in the GATEWAY (trade mark) manual.

For example, one route is to insert a generic polylinker into the Entry Vector, in which the inserted DNA contains two *att* sites separated by the polylinker sequence. This approach facilitates insertion of a variety of fragments into the Entry Vector, at user-defined restriction endonuclease sites.

A second route is to insert *att* sites into the primers used for amplification of the DNA of interest. In this approach, the DNA sequence of the amplified fragment is modified to include the appropriate *att* sites at the 5' and 3' ends.

Examples of Entry Vectors are provided for LH_N/C (SEQ ID 135), for LH_N/C with no STOP codon thereby facilitating direct fusion to ligands (SEQ ID 136), and for a L-chain/C sequence that can facilitate combination with an appropriate second or third domain (SEQ ID 134).

By combination of the modified Entry Vector (containing the DNA of interest) and a Destination Vector of choice, an expression clone is generated. The Destination Vector typically provides the necessary information to facilitate transcription of the inserted DNA of interest and, when introduced into an appropriate host cell, facilitates expression of protein.

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Destination Vectors may be prepared to ensure expression of N-terminal and/or C-terminal fusion tags and/or additional protein domains. An example of a novel engineered Destination Vector for the expression of MBP-tagged proteins in a non-transmissible vector backbone is presented in SEQ ID 137. In this specific embodiment, recombination of an Entry Vector possessing a sequence of interest with the Destination vector identified in SEQ ID 137 results in an expression vector for *E. coli* expression.

The combination of Entry and Destination Vectors to prepare an expression clone results in an expressed protein that has a modified sequence. In the Examples illustrated with SEQ ID 30 & 124, a peptide sequence of TSLYKKAGF is to be found at the N-terminus of the endopeptidase following cleavage to remove the purification tag. This peptide sequence is encoded by the DNA that forms the *att* site and is a feature of all clones that are constructed and expressed in this way.

It will be appreciated that the *att* site sequence may be modified to insert DNA encoding a specific protease cleavage site (for example from Table 1) to the 3' of the *att* site of the entry clone.

It will be also appreciated that the precise N-terminus of any polypeptide (eg. a LHN fragment) will vary depending on how the endopeptidase DNA was introduced into the entry vector and its relationship to the 5' *att* site. SEQ ID 29/30 & 123/124 are a case in point. The N-terminal extension of SEQ ID 30 is TSLYKKAGFGS whereas the N-terminal extension of SEQ ID 124 is ITSLYKKAGFGSLDH. These amino acid extension-containing domains provide further examples of first/second domain variants according to the present invention.

Within the context of the present invention, the following definitions are to be noted.

The term polypeptide "fragment" means that the polypeptide "fragment" in question is preferably at least 50% the length of the reference SEQ ID polypeptide sequence.

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Thus, if the reference SEQ ID polypeptide is an amino acid sequence having for example 500 amino acid residues, then the corresponding "fragment" would be an amino acid sequence having at least 250 amino acid residues. In more preferred embodiments, the "fragment" is at least 70%, more preferably at least 85%, particularly preferably at least 90% and most preferably at least 95% the length of the reference SEQ ID polypeptide.

The polypeptide "fragment" preferably includes an epitope of the reference SEQ ID polypeptide sequence, which may be confirmed by antibody cross-reactivity. The polypeptide "fragment" preferably includes a first domain that is capable of cleaving one or more vesicle or plasma membrane associated proteins essential to exocytosis..

The term "variant" means a polypeptide or polypeptide "fragment" having at least seventy, preferably at least eighty, more preferably at least ninety percent amino acid sequence homology with the reference SEQ ID polypeptide. An example of a "variant" is a polypeptide or polypeptide fragment that contains one or more analogues of an amino acid (eg. an unnatural amino acid), or a substituted linkage. The terms "homology" and "identity" are considered synonymous in this specification.

For sequence comparison, typically one sequence (eg. the reference SEQ ID polypeptide) acts as a reference sequence, to which "variant" sequences may be compared. When using a sequence comparison algorithm, "variant" and reference sequences are input into a computer, subsequent coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percentage sequence identity for the "variant" sequence(s) relative to the reference SEQ ID polypeptide sequence, based on the designated program parameters.

Optimal alignment of sequences for comparison may be conducted, for example, by the local homology alignment algorithm of Smith and Waterman [Adv. Appl. Math. 2: 484 (1981)], by the algorithm of Needleman & Wunsch [J. Mol. Biol. 48: 443 (1970)] by the search for similarity method of Pearson & Lipman [Proc. Nat'l. Acad. Sci. USA 85: 2444

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(1988)], by computer implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA - Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, Wis. 53705); or by visual inspection [see Current Protocols in Molecular Biology, F.M. Ausbel et al; eds, Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc. (1995 Supplement) Ausbubel].

Examples of algorithms suitable for determining percent sequence similarity are the BLAST and BLAST 2.0 algorithms [see Altschul (1990) J. Mol. Biol. 215: pp. 403-410; and "<http://www.ncbi.nlm.nih.gov/>" of the National Center for Biotechnology Information].

In a preferred homology comparison, the identity exists over a region of the sequences that is at least 50 amino acid residues in length, more preferably at least 100 amino acid residues in length, particularly preferably at least 150 amino acid residues in length, and most preferably at least 200 amino acid residues in length. Alternatively, the identity exists over the entire sequence of, for example, the "variant" polypeptide.

The term DNA "fragment" used in this invention is to be interpreted consistently with the term polypeptide "fragment" (discussed above), and means that the DNA "fragment" in question is preferably at least 50% the length of the reference SEQ ID DNA sequence. Thus, if the reference SEQ ID DNA sequence is a nucleic acid sequence having for example 500 nucleotide residues, then the corresponding "fragment" would be a nucleic acid sequence having at least 250 nucleotide residues. In more preferred embodiments, the "fragment" is at least 70%, more preferably at least 85%, particularly preferably at least 90% and most preferably at least 95% the length of the reference SEQ ID DNA sequence.

The term DNA "variant" means a DNA sequence that has substantial homology or substantial similarity to the reference DNA sequence (or a fragment thereof). A nucleic acid or fragment thereof is "substantially homologous" (or "substantially similar") to another if, when optimally aligned (with appropriate nucleotide insertions or deletions) with the other nucleic acid (or its complementary strand), there is nucleotide sequence

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identity in at least about 60% of the nucleotide bases, usually at least about 70%, more usually at least about 80%, preferably at least about 90%, and more preferably at least about 95 to 98% of the nucleotide bases. Homology determination is performed as described *supra* for peptides.

Alternatively, a DNA "variant" is substantially homologous (or substantially similar) with the coding sequence (or a fragment thereof) of reference SEQ ID DNA sequence when they are capable of hybridizing under selective hybridization conditions. Selectivity of hybridization exists when hybridization occurs which is substantially more selective than total lack of specificity. Typically, selective hybridization will occur when there is at least about 65% homology over a stretch of at least about 50 nucleotides, preferably at least about 70%, more preferably at least about 75%, and most preferably at least about 90%. See, Kanehisa (1984) Nuc. Acids Res. 12:203-213. The length of homology comparison, as described, may be over longer stretches, and in certain embodiments will often be over a stretch of at least about 100 nucleotides, usually at least about 150 nucleotides, more usually at least about 200 nucleotides, typically at least about 250 nucleotides, more typically at least about 300 nucleotides, and preferably at least about 350 or more nucleotides. Alternatively, the identity exists over the entire sequence of, for example, the "variant" DNA sequence.

Nucleic acid hybridization will be affected by such conditions as salt concentration (eg. NaCl), temperature, or organic solvents, in addition to the base composition, length of the complementary strands, and the number of nucleotide base mismatches between the hybridizing nucleic acids, as will be readily appreciated by those skilled in the art. Stringent temperature conditions are preferably employed, and generally include temperatures in excess of 30°C, typically in excess of 37°C and preferably in excess of 45°C. Stringent salt conditions will ordinarily be less than 1000 mM, typically less than 500 mM, and preferably less than 200 mM. The pH is typically between 7.0 and 8.3. However, the combination of parameters is much more important than the measure of any single parameter. See, eg., Wetmur and Davidson (1968) J. Mol. Biol. 31:349-370.

The above terms DNA "fragment" and "variant" have in common with each other that

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the resulting polypeptide products preferably have cross-reactive antigenic properties which are substantially the same as those of the corresponding reference SEQ ID polypeptide. Preferably all of the polypeptide products of the above DNA "fragment" and "variant" embodiments of the present invention bind to an antibody which also binds to the reference SEQ ID polypeptide.

There now follows description of specific embodiments of the invention, illustrated by drawings in which:

Fig. 1 shows a schematic representation of the domain structure of botulinum neurotoxin type A (BoNT/A);

Fig. 2 shows a schematic representation of assembly of the gene for an embodiment of the invention designated LH₄₂₃/A;

Fig. 3 is a graph comparing activity of native toxin, trypsin generated "native" LH_N/A and an embodiment of the invention designated ₂LH₄₂₃/A (Q₂E,N₂₆K,A₂₇Y) in an *in vitro* peptide cleavage assay;

Fig. 4 is a comparison of the first 33 amino acids in published sequences of native toxin and embodiments of the invention;

Fig. 5 shows the transition region of an embodiment of the invention designated L₄H₄₂₃/A illustrating insertion of four amino acids at the N-terminus of the H_N sequence; amino acids coded for by the *Eco* 47 III restriction endonuclease cleavage site are marked and the H_N sequence then begins ALN...;

Fig. 6 shows the transition region of an embodiment of the invention designated L_{FXa/3}H₄₂₃/A illustrating insertion of a Factor Xa cleavage site at the C-terminus of the L-chain, and three additional amino acids coded for at the N-terminus of the H-sequence; the N-terminal amino acid of the cleavage-

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activated H_N will be cysteine;

Fig. 7 shows the C-terminal portion of the amino acid sequence of an embodiment of the invention designated L_{FXa/3}H₄₂₃/A-IGF-1, a fusion protein; the IGF-1 sequence begins at position G₈₈₂;

Fig. 8 shows the C-terminal portion of the amino acid sequence of an embodiment of the invention designated L_{FXa/3}H₄₂₃/A-CtxA14, a fusion protein; the C-terminal-CtxA sequence begins at position Q₈₈₂;

Fig. 9 shows the C-terminal portion of the amino acid sequence of an embodiment of the invention designated L_{FXa/3}H₄₂₃/A-ZZ, a fusion protein; the C-terminal ZZ sequence begins at position A₈₉₀ immediately after a genenase recognition site (underlined);

Figs. 10 & 11 show schematic representations of manipulations of polypeptides of the invention; Fig. 10 shows LH₄₂₃/A with N-terminal addition of an affinity purification peptide (in this case GST) and C-terminal addition of an Ig binding domain; protease cleavage sites R1, R2 and R3 enable selective enzymatic separation of domains; Fig. 11 shows specific examples of protease cleavage sites R1, R2 and R3 and a C-terminal fusion peptide sequence;

Fig. 12 shows the trypsin sensitive activation region of a polypeptide of the invention;

Fig. 13 shows Western blot analysis of recombinant LH₁₀₇/B expressed from *E.coli*; panel A was probed with anti-BoNT/B antiserum; Lane 1, molecular weight standards; lanes 2 & 3, native BoNT/B; lane 4, immunopurified LH₁₀₇/B; panel B was probed with anti-T7 peptide tag antiserum; lane 1, molecular weight standards; lanes 2 & 3, positive control *E.coli* T7 expression; lane 4 immunopurified LH₁₀₇/B.

Fig. 14

illustrates a fusion protein of the present invention, which fusion protein includes two different proteolytic cleavage sites (E1, and E2) between a purification tag (TAG) and a first domain (L-chain), and a duplicate proteolytic cleavage sites (E2) between a first domain (L-chain) and a second domain (H_N). Use of the E2 protease results in simultaneous cleavage at the two defined E2 cleavage sites leaving a dichain polypeptide molecule comprising the first and second domains, whereas use of the E1 protease results in cleavage at the single defined E1 cleavage site leaving a single polypeptide chain molecule comprising the first and second domains.

Fig. 15

illustrates the use of molecular-clamping technology to fuse together a polypeptide comprising first and second domains (eg. LH_N), and a second molecule comprising a third domain (eg. a ligand).

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The sequence listing that accompanies this application contains the following sequences:-

<u>SEQ ID NO:</u>	<u>Sequence</u>
1	DNA coding for LH ₄₂₃ /A
2	LH ₄₂₃ /A
3	DNA coding for ₂₃ LH ₄₂₃ /A (Q ₂ E,N ₂₆ K,A ₂₇ Y), of which an N-terminal portion is shown in Fig. 4.
4	₂₃ LH ₄₂₃ /A (Q ₂ E,N ₂₆ K,A ₂₇ Y)
5	DNA coding for ₂ LH ₄₂₃ /A (Q ₂ E,N ₂₆ K,A ₂₇ Y), of which an N-terminal portion is shown in Fig.4
6	₂ LH ₄₂₃ /A (Q ₂ E,N ₂₆ K,A ₂₇ Y)
7	DNA coding for native BoNT/A according to Binz et al
8	native BoNT/A according to Binz et al
9	DNA coding for L _{/4} H ₄₂₃ /A
10	L _{/4} H ₄₂₃ /A
11	DNA coding for L _{FXa/3} H ₄₂₃ /A
12	L _{FXa/3} H ₄₂₃ /A
13	DNA coding for L _{FXa/3} H ₄₂₃ /A-IGF-1

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- 14 L_{FXa/3}H₄₂₃/A-IGF-1
- 15 DNA coding for L_{FXa/3}H₄₂₃/A-CtxA14
- 16 L_{FXa/3}H₄₂₃/A-CtxA14
- 17 DNA coding for L_{FXa/3}H₄₂₃/A-ZZ
- 18 L_{FXa/3}H₄₂₃/A-ZZ
- 19 DNA coding for LH₇₂₈/B
- 20 LH₇₂₈/B
- 21 DNA coding for LH₄₁₇/B
- 22 LH₄₁₇/B
- 23 DNA coding for LH₁₀₇/B
- 24 LH₁₀₇/B
- 25 DNA coding for LH₄₂₃/A (Q₂E,N₂₆K,A₂₇Y)
- 26 LH₄₂₃/A (Q₂E,N₂₆K,A₂₇Y)
- 27 DNA coding for LH₄₁₇/B wherein the first 274 bases are modified to have an *E.coli* codon bias
- 28 DNA coding for LH₄₁₇/B wherein bases 691-1641 of the native BoNT/B sequence have been replaced by a

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degenerate DNA coding for amino acid residues 231-547 of the native BoNT/B polypeptide

29 DNA coding for LH_N/A as expressed from a Gateway adapted destination vector. LH_N/A incorporates an enterokinase activation site at the LC-H_N junction and an 11 amino acid *att* site peptide extension at the 5' end of the LH_N/A sequence

30 LH_N/A produced by expression of SEQ ID 29, said polypeptide incorporating an enterokinase activation site at the LC-H_N junction and an 11 amino acid *att* site peptide extension at the N-terminus of the LH_N/A sequence

31 DNA coding for LH_N/A with an enterokinase activation site at the LC-H_N junction

32 LH_N/A produced by expression of SEQ ID 31, said polypeptide having an enterokinase activation site at the LC-H_N junction

33 DNA coding for LH_N/A with a Factor Xa protease activation site at the LC-H_N junction

34 LH_N/A produced by expression of SEQ ID 33, said polypeptide having a Factor Xa protease activation site at the LC-H_N junction

35 DNA coding for LH_N/A with a Precision protease activation site at the LC-H_N junction

36 LH_N/A produced by expression of SEQ ID 35, said

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polypeptide having a Precision protease activation site at the LC-H_N junction

- 37 DNA coding for LH_N/A with a Thrombin protease activation site at the LC-H_N junction
- 38 LH_N/A produced by expression of SEQ ID 37, said polypeptide having a Thrombin protease activation site at the LC-H_N junction
- 39 DNA coding for an LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion in which the LC-H_N junction does not incorporate a specific protease cleavage site and the ligand is spaced from the H_N domain by a (GGGGS)₃ spacer.
- 40 LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion produced by expression of SEQ ID 39, in which the LC-H_N junction does not incorporate a specific protease cleavage site and the ligand is spaced from the H_N domain by a (GGGGS)₃ spacer.
- 41 DNA coding for LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion in which the LC-H_N junction does not incorporate a specific protease cleavage site and the ligand is spaced from the H_N domain by a helical spacer.
- 42 LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion produced by expression of SEQ ID 41, in which the LC-H_N junction does not incorporate a specific protease cleavage site and the ligand is spaced from the H_N domain by a helical spacer.
- 43 DNA coding for LH_N/A-ligand (*Erythrina cristagalli* lectin)

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fusion in which the LC-H_N junction incorporates a specific enterokinase protease activation site and the ligand is spaced from the H_N domain by a (GGGGS)₃ spacer.

44

LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion produced by expression of SEQ ID 43, in which the LC-H_N junction incorporates a specific enterokinase protease activation site and the ligand is spaced from the H_N domain by a (GGGGS)₃ spacer.

45

DNA coding for LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion in which the LC-H_N junction incorporates a specific enterokinase protease activation site and the ligand is spaced from the H_N domain by a helical spacer.

46

LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion produced by expression of SEQ ID 45, in which the LC-H_N junction incorporates a specific enterokinase protease activation site and the ligand is spaced from the H_N domain by a helical spacer.

47

DNA coding for LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion in which the LC-H_N junction incorporates a specific Thrombin protease activation site and the ligand is spaced from the H_N domain by a helical spacer.

48

LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion produced by expression of SEQ ID 47, in which the LC-H_N junction incorporates a specific Thrombin protease activation site and the ligand is spaced from the H_N domain by a helical spacer.

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- 49 DNA coding for LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion in which the LC-H_N junction incorporates a specific Thrombin protease activation site and the ligand is spaced from the H_N domain by a (GGGGS)₃ spacer.
- 50 LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion produced by expression of SEQ ID 49, in which the LC-H_N junction incorporates a specific Thrombin protease activation site and the ligand is spaced from the H_N domain by a (GGGGS)₃ spacer.
- 51 DNA coding for LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion in which the LC-H_N junction incorporates a specific Precision protease activation site and the ligand is spaced from the H_N domain by a helical spacer.
- 52 LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion produced by expression of SEQ ID 51, in which the LC-H_N junction incorporates a specific Precision protease activation site and the ligand is spaced from the H_N domain by a helical spacer.
- 53 DNA coding for LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion in which the LC-H_N junction incorporates a specific Precision protease activation site and the ligand is spaced from the H_N domain by a (GGGGS)₃ spacer.
- 54 LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion produced by expression of SEQ ID 53, in which the LC-H_N junction incorporates a specific Precision protease activation site and the ligand is spaced from the H_N domain by a (GGGGS)₃ spacer.

- 55 DNA coding for LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion in which the LC-H_N junction incorporates a specific Factor Xa protease activation site and the ligand is spaced from the H_N domain by a helical spacer.
- 56 LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion produced by expression of SEQ ID 55, in which the LC-H_N junction incorporates a specific Factor Xa protease activation site and the ligand is spaced from the H_N domain by a helical spacer.
- 57 DNA coding for LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion in which the LC-H_N junction incorporates a specific Factor Xa protease activation site and the ligand is spaced from the H_N domain by a (GGGGS)₃ spacer.
- 58 LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion produced by expression of SEQ ID 57, in which the LC-H_N junction incorporates a specific Factor Xa protease activation site and the ligand is spaced from the H_N domain by a (GGGGS)₃ spacer.
- 59 DNA coding for LH_N/A incorporating an enterokinase protease activation site at the LC-H_N junction and a C-terminal *fos* ligand bounded by a pair of Cys residues
- 60 LH_N/A produced by expression of SEQ ID 59, said polypeptide incorporating an enterokinase protease activation site at the LC-H_N junction and a C-terminal *fos* ligand bounded by a pair of Cys residues

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- 61 DNA coding for LH_N/A incorporating an enterokinase protease activation site at the LC-H_N junction and a C-terminal (Glu)₈ peptide bounded by a pair of Cys residues
- 62 LH_N/A produced by expression of SEQ ID 61, said polypeptide incorporating an enterokinase protease activation site at the LC-H_N junction and a C-terminal (Glu)₈ peptide bounded by a pair of Cys residues
- 63 DNA coding for LH_N/A incorporating an enterokinase protease activation site at the LC-H_N junction and a C-terminal *fos* ligand
- 64 LH_N/A produced by expression of SEQ ID 63, said polypeptide incorporating an enterokinase protease activation site at the LC-H_N junction and a C-terminal *fos* ligand
- 65 DNA coding for LH_N/A incorporating an enterokinase protease activation site at the LC-H_N junction and a C-terminal (Glu)₈ peptide
- 66 LH_N/A produced by expression of SEQ ID 65, said polypeptide incorporating an enterokinase protease activation site at the LC-H_N junction and a C-terminal (Glu)₈ peptide
- 67 DNA coding for LH_N/A incorporating an enterokinase protease activation site at the LC-H_N junction and a C-terminal self-cleavable intein polypeptide to facilitate thioester formation for use in chemical directed coupling

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- 68 LH_N/A produced by expression of SEQ ID 67, said polypeptide incorporating an enterokinase protease activation site at the LC-H_N junction and a C-terminal self-cleavable intein polypeptide to facilitate thioester formation for use in chemical directed coupling
- 69 DNA coding for LC/A with no STOP codon, a linker peptide incorporating the first 6 amino acids of the H_N domain and an enterokinase cleavage site.
- 70 LC/A produced by expression of SEQ ID 69, said polypeptide having no STOP codon, a linker peptide incorporating the first 6 amino acids of the H_N domain and an enterokinase cleavage site.
- 71 DNA coding for LC/A with no STOP codon, a linker peptide incorporating the first 6 amino acids of the H_N domain and an Factor Xa cleavage site.
- 72 LC/A produced by expression of SEQ ID 71, said polypeptide having no STOP codon, a linker peptide incorporating the first 6 amino acids of the H_N domain and an Factor Xa cleavage site.
- 73 DNA coding for LC/A with no STOP codon and a linker peptide representing the native LC-H_N sequence incorporating the first 6 amino acids of the H_N domain
- 74 LC/A produced by expression of SEQ ID 73, said polypeptide having no STOP codon and a linker peptide representing the native LC-H_N sequence incorporating the first 6 amino acids of the H_N domain

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- 75 DNA coding for LC/A with no STOP codon, a linker peptide incorporating the first 6 amino acids of the H_N domain and an Precision cleavage site.
- 76 LC/A produced by expression of SEQ ID 75, said polypeptide having no STOP codon, a linker peptide incorporating the first 6 amino acids of the H_N domain and an Precision cleavage site.
- 77 DNA coding for LC/A with no STOP codon, a linker peptide incorporating the first 6 amino acids of the H_N domain and an Thrombin cleavage site.
- 78 LC/A produced by expression of SEQ ID 77, said polypeptide having no STOP codon, a linker peptide incorporating the first 6 amino acids of the H_N domain and an Thrombin cleavage site.
- 79 DNA coding for LH_N/B incorporating an enterokinase protease activation site at the LC-H_N junction (in which there are 11 amino acids between the Cys residues of the LC & H_N domains) and a 6 amino acid N-terminal extension
- 80 LH_N/B produced by expression of SEQ ID 79, said polypeptide incorporating an enterokinase protease activation site at the LC-H_N junction (in which there are 11 amino acids between the Cys residues of the LC & H_N domains) and a 6 amino acid N-terminal extension
- 81 DNA coding for LH_N/B incorporating an enterokinase protease activation site at the LC-H_N junction (in which

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there are 20 amino acids between the Cys residues of the LC & H_N domains) and a 6 amino acid N-terminal extension

82 LH_N/B produced by expression of SEQ ID 82, said polypeptide incorporating an enterokinase protease activation site at the LC-H_N junction (in which there are 20 amino acids between the Cys residues of the LC & H_N domains) and a 6 amino acid N-terminal extension

83 DNA coding for LH_N/B incorporating a Factor Xa protease activation site at the LC-H_N junction and an 11 amino acid N-terminal extension resulting from cleavage at an intein self-cleaving polypeptide

84 LH_N/B produced by expression of SEQ ID 83, said polypeptide incorporating a Factor Xa protease activation site at the LC-H_N junction and an 11 amino acid N-terminal extension resulting from cleavage at an intein self-cleaving polypeptide

85 DNA coding for LH_N/B incorporating a Factor Xa protease activation site at the LC-H_N junction and an 11 amino acid N-terminal extension (retaining a Factor Xa protease cleavage site) resulting from cleavage at a TEV protease cleavage site (included to release the LH_N/B from a purification tag).

86 LH_N/B produced by expression of SEQ ID 85, said polypeptide incorporating a Factor Xa protease activation site at the LC-H_N junction and an 11 amino acid N-terminal extension (retaining a Factor Xa protease cleavage site) resulting from cleavage at a TEV protease cleavage site

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(included to release the LH_N/B from a purification tag).

87 DNA coding for LH_N/B incorporating a Factor Xa protease activation site at the LC-H_N junction and a 6 amino acid N-terminal extension

88 LH_N/B produced by expression of SEQ ID 87, said polypeptide incorporating a Factor Xa protease activation site at the LC-H_N junction and a 6 amino acid N-terminal extension

89 DNA coding for LH_N/B incorporating a Factor Xa protease activation site at the LC-H_N junction and an 11 amino acid N-terminal extension (retaining an enterokinase protease cleavage site) resulting from cleavage at a Factor Xa protease cleavage site (included to release the LH_N/B from a purification tag).

90 LH_N/B produced by expression of SEQ ID 89, said polypeptide incorporating a Factor Xa protease activation site at the LC-H_N junction and an 11 amino acid N-terminal extension (retaining an enterokinase protease cleavage site) resulting from cleavage at a Factor Xa protease cleavage site (included to release the LH_N/B from a purification tag).

91 DNA coding for LH_N/B incorporating a Factor Xa protease activation site at the LC-H_N junction and an 10 amino acid N-terminal extension (retaining a Factor Xa protease cleavage site) resulting from cleavage at an enterokinase protease cleavage site (included to release the LH_N/B from a purification tag).

- 92 LH_N/B produced by expression of SEQ ID 91, said polypeptide incorporating a Factor Xa protease activation site at the LC-H_N junction and an 10 amino acid N-terminal extension (retaining a Factor Xa protease cleavage site) resulting from cleavage at an enterokinase protease cleavage site (included to release the LH_N/B from a purification tag).
- 93 DNA coding for LH_N/B incorporating a Factor Xa protease activation site at the LC-H_N junction and a 2 amino acid (Gly-Ser) N-terminal extension as expressed in pGEX-4T-2
- 94 LH_N/B produced by expression of SEQ ID 93, said polypeptide incorporating a Factor Xa protease activation site at the LC-H_N junction and a 2 amino acid (Gly-Ser) N-terminal extension as expressed in pGEX-4T-2
- 95 DNA coding for LH_N/B incorporating a Factor Xa protease activation site at the LC-H_N junction and a 7 amino acid (Ser-Pro-Gly-Ala-Arg-Gly-Ser) N-terminal extension as expressed in pET-43a
- 96 LH_N/B produced by expression of SEQ ID 95, said polypeptide incorporating a Factor Xa protease activation site at the LC-H_N junction and a 7 amino acid (Ser-Pro-Gly-Ala-Arg-Gly-Ser) N-terminal extension as expressed in pET-43a
- 97 DNA coding for LH_N/B incorporating a Factor Xa protease activation site at the LC-H_N junction and a 7 amino acid (Ala-Met-Ala-Glu-Ile-Gly-Ser) N-terminal extension as

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expressed in pET-32a

- 98 LH_N/B produced by expression of SEQ ID 97, said polypeptide incorporating a Factor Xa protease activation site at the LC-H_N junction and a 7 amino acid (Ala-Met-Ala-Asp-Ile-Gly-Ser) N-terminal extension as expressed in pET-32a
- 99 DNA coding for LH_N/B incorporating a Thrombin protease activation site at the LC-H_N junction and a 6 amino acid (Ile-Ser-Glu-Phe-Gly-Ser) N-terminal extension as expressed in pMAL-c2
- 100 LH_N/B produced by expression of SEQ ID 99, said polypeptide incorporating a Thrombin protease activation site at the LC-H_N junction and a 6 amino acid (Ile-Ser-Glu-Phe-Gly-Ser) N-terminal extension as expressed in pMAL-c2
- 101 DNA coding for LH_N/B incorporating a TEV protease activation site at the LC-H_N junction and a 6 amino acid (Ile-Ser-Glu-Phe-Gly-Ser) N-terminal extension as expressed in pMAL-c2
- 102 LH_N/B produced by expression of SEQ ID 101, said polypeptide incorporating a TEV protease activation site at the LC-H_N junction and a 6 amino acid (Ile-Ser-Glu-Phe-Gly-Ser) N-terminal extension as expressed in pMAL-c2
- 103 DNA coding for LH_N/B incorporating a Factor Xa protease activation site at the LC-H_N junction and a 6 amino acid (Ile-Ser-Glu-Phe-Gly-Ser) N-terminal extension as expressed in

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pMAL-c2. DNA incorporates *MfeI* and *AvrII* restriction enzyme sites for incorporation of novel linker sequences at the LC-H_N junction.

- 104 LH_N/B produced by expression of SEQ ID 103, said polypeptide incorporating a Factor Xa protease activation site at the LC-H_N junction and a 6 amino acid (Ile-Ser-Glu-Phe-Gly-Ser) N-terminal extension as expressed in pMAL-c2.
- 105 DNA coding for LH_N/B incorporating an enterokinase protease activation site at the LC-H_N junction (in which there are 20 amino acids between the Cys residues of the LC & H_N domains) and a 6 amino acid (Ile-Ser-Glu-Phe-Gly-Ser) N-terminal extension. *AvrII* restriction site is deleted.
- 106 LH_N/B produced by expression of SEQ ID 105, said polypeptide incorporating an enterokinase protease activation site at the LC-H_N junction (in which there are 20 amino acids between the Cys residues of the LC & H_N domains) and a 6 amino acid (Ile-Ser-Glu-Phe-Gly-Ser) N-terminal extension
- 107 DNA coding for LH_N/B incorporating an enterokinase protease activation site at the LC-H_N junction (in which there are 20 amino acids between the Cys residues of the LC & H_N domains) and a 6 amino acid (Ile-Ser-Glu-Phe-Gly-Ser) N-terminal extension.
- 108 LH_N/B produced by expression of SEQ ID 107, said polypeptide incorporating an enterokinase protease

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activation site at the LC-H_N junction (in which there are 20 amino acids between the Cys residues of the LC & H_N domains) and a 6 amino acid (Ile-Ser-Glu-Phe-Gly-Ser) N-terminal extension.

109

DNA coding for a maltose-binding protein-Factor Xa-intein-LC/B-Factor Xa-H_N expression construct.

110

MBP-LH_N/B produced by expression of SEQ ID 109, said polypeptide incorporating a self-cleavable intein sequence to facilitate removal of the MBP purification tag and a Factor Xa protease activation site at the LC-H_N junction

111

DNA coding for LH_N/B incorporating an enterokinase protease activation site at the LC-H_N junction (in which there are 11 amino acids between the Cys residues of the LC & H_N domains) and an 11 amino acid (Thr-Ser-Leu-Tyr-Lys-Lys-Ala-Gly-Phe-Gly-Ser) N-terminal extension derived from the *att* site adaptation of the vector. This construct has the C-terminal STOP codon removed to facilitate direct fusion of fragment and ligands.

112

LH_N/B produced by expression of SEQ ID 111, said polypeptide incorporating an enterokinase protease activation site at the LC-H_N junction (in which there are 11 amino acids between the Cys residues of the LC & H_N domains) and an 11 amino acid (Thr-Ser-Leu-Tyr-Lys-Lys-Ala-Gly-Phe-Gly-Ser) N-terminal extension derived from the *att* site adaptation of the vector.

113

DNA coding for LC/B with no STOP codon, a linker peptide incorporating the first 6 amino acids of the H_N domain and

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an enterokinase protease cleavage site bounded by Cys residues

- 114 LC/B produced by expression of SEQ ID 113, said polypeptide having no STOP codon, a linker peptide incorporating the first 6 amino acids of the H_N domain and an enterokinase protease cleavage site bounded by Cys residues
- 115 DNA coding for LH_N/C incorporating a Factor Xa cleavage site at the LC-H_N junction, an 11 amino acid (Thr-Ser-Leu-Tyr-Lys-Lys-Ala-Gly-Phe-Gly-Ser) N-terminal extension derived from the *att* site adaptation of the vector, and a C-terminal (Glu)₈ peptide to facilitate molecular clamping.
- 116 LH_N/C produced by expression of SEQ ID 115, said polypeptide incorporating a Factor Xa cleavage site at the LC-H_N junction, an 11 amino acid (Thr-Ser-Leu-Tyr-Lys-Lys-Ala-Gly-Phe-Gly-Ser) N-terminal extension derived from the *att* site adaptation of the vector, and a C-terminal (Glu)₈ peptide to facilitate molecular clamping.
- 117 DNA coding for LH_N/C incorporating a Factor Xa cleavage site at the LC-H_N junction, an 11 amino acid (Thr-Ser-Leu-Tyr-Lys-Lys-Ala-Gly-Phe-Gly-Ser) N-terminal extension derived from the *att* site adaptation of the vector, and a C-terminal *fos* ligand bounded by a pair of Cys residues to facilitate molecular clamping.
- 118 LH_N/C produced by expression of SEQ ID 117, said polypeptide incorporating a Factor Xa cleavage site at the LC-H_N junction, an 11 amino acid (Thr-Ser-Leu-Tyr-Lys-

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Lys-Ala-Gly-Phe-Gly-Ser) N-terminal extension derived from the *att* site adaptation of the vector, and a C-terminal *fos* ligand bounded by a pair of Cys residues to facilitate molecular clamping.

119

DNA coding for LH_N/C incorporating a Factor Xa cleavage site at the LC-H_N junction, an 11 amino acid (Thr-Ser-Leu-Tyr-Lys-Lys-Ala-Gly-Phe-Gly-Ser) N-terminal extension derived from the *att* site adaptation of the vector, and a C-terminal (Glu)₈ peptide bounded by a pair of Cys residues to facilitate molecular clamping

120

LH_N/C produced by expression of SEQ ID 119, said polypeptide incorporating a Factor Xa cleavage site at the LC-H_N junction, an 11 amino acid (Thr-Ser-Leu-Tyr-Lys-Lys-Ala-Gly-Phe-Gly-Ser) N-terminal extension derived from the *att* site adaptation of the vector, and a C-terminal (Glu)₈ peptide bounded by a pair of Cys residues to facilitate molecular clamping

121

DNA coding for LH_N/C incorporating a Factor Xa cleavage site at the LC-H_N junction, an 11 amino acid (Thr-Ser-Leu-Tyr-Lys-Lys-Ala-Gly-Phe-Gly-Ser) N-terminal extension derived from the *att* site adaptation of the vector, and a C-terminal *fos* ligand to facilitate molecular clamping.

122

LH_N/C produced by expression of SEQ ID 121, said polypeptide incorporating a Factor Xa cleavage site at the LC-H_N junction, an 11 amino acid (Thr-Ser-Leu-Tyr-Lys-Lys-Ala-Gly-Phe-Gly-Ser) N-terminal extension derived from the *att* site adaptation of the vector, and a C-terminal *fos* ligand to facilitate molecular clamping

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- 123 DNA coding for LH_N/C incorporating a Factor Xa cleavage site at the LC-H_N junction, a 15 amino acid (Ile-Thr-Ser-Leu-Tyr-Lys-Lys-Ala-Gly-Phe-Gly-Ser-Leu-Asp-His) N-terminal extension derived from the *att* site adaptation of the vector.
- 124 LH_N/C produced by expression of SEQ ID 123, said polypeptide incorporating a Factor Xa cleavage site at the LC-H_N junction, a 15 amino acid (Ile-Thr-Ser-Leu-Tyr-Lys-Lys-Ala-Gly-Phe-Gly-Ser-Leu-Asp-His) N-terminal extension derived from the *att* site adaptation of the vector.
- 125 DNA coding for LH_N/C incorporating a Factor Xa cleavage site at the LC-H_N junction and an 11 amino acid (Val-Pro-Glu-Phe-Gly-Ser-Ser-Arg-Val-Asp-His) N-terminal extension derived following cleavage of the protein with enterokinase
- 126 LH_N/C produced by expression of SEQ ID 125, said polypeptide incorporating a Factor Xa cleavage site at the LC-H_N junction and an 11 amino acid (Val-Pro-Glu-Phe-Gly-Ser-Ser-Arg-Val-Asp-His) N-terminal extension derived following cleavage of the protein with enterokinase to release the N-terminal MBP purification tag.
- 127 DNA coding for LH_N/C incorporating a Factor Xa cleavage site at the LC-H_N junction and an 10 amino acid (Val-Glu-Phe-Gly-Ser-Ser-Arg-Val-Asp-His) N-terminal extension derived following cleavage of the protein with genenase
- 128 LH_N/C produced by expression of SEQ ID 127, said polypeptide incorporating a Factor Xa cleavage site at the

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LC-H_N junction and an 10 amino acid (Val-Glu-Phe-Gly-Ser-Ser-Arg-Val-Asp-His) N-terminal extension derived following cleavage of the protein with genenase to release the N-terminal MBP purification tag

129 DNA coding for LH_N/C incorporating a Factor Xa cleavage site at the LC-H_N junction and an 11 amino acid (Ile-Ser-Glu-Phe-Gly-Ser-Ser-Arg-Val-Asp-His) N-terminal extension derived following cleavage of the protein with Factor Xa

130 LH_N/C produced by expression of SEQ ID 129, said polypeptide incorporating a Factor Xa cleavage site at the LC-H_N junction and an 11 amino acid (Ile-Ser-Glu-Phe-Gly-Ser-Ser-Arg-Val-Asp-His) N-terminal extension derived following cleavage of the protein with Factor Xa

131 DNA coding for LH_N/C incorporating a Factor Xa cleavage site at the LC-H_N junction, a 15 amino acid (Ile-Thr-Ser-Leu-Tyr-Lys-Lys-Ala-Gly-Phe-Gly-Ser-Leu-Asp-His) N-terminal extension and a 21 amino acid (Leu-Gln-Thr-Leu-Asp-Asp-Pro-Ala-Phe-Leu-Tyr-Lys-Val-Val-Ile-Phe-Gln-Asn-Ser-Asp-Pro) C-terminal extension derived from the *att* site adaptation of the vector. The clone has no STOP codon in order to facilitate fusion of ligands onto C-terminus of H_N domain.

132 LH_N/C produced by expression of SEQ ID 131, said polypeptide incorporating a Factor Xa cleavage site at the LC-H_N junction, a 15 amino acid (Ile-Thr-Ser-Leu-Tyr-Lys-Lys-Ala-Gly-Phe-Gly-Ser-Leu-Asp-His) N-terminal extension and a 21 amino acid (Leu-Gln-Thr-Leu-Asp-Asp-Pro-Ala-Phe-Leu-Tyr-Lys-Val-Val-Ile-Phe-Gln-Asn-Ser-Asp-

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Pro) C-terminal extension derived from the *att* site adaptation of the vector. The clone has no STOP codon in order to facilitate fusion of ligands onto C-terminus of H_N domain.

133

DNA coding for LH_N/C incorporating a Factor Xa cleavage site at the LC-H_N junction, an N-terminal extension and a C-terminal extension derived from the *att* site adaptation of the vector. The clone has no STOP codon in order to facilitate fusion of ligands onto C-terminus of H_N domain.

134

DNA coding for LC/C as prepared in pENTRY2 for use in the Gateway site specific recombination cloning system. LC/C has no STOP codon in order to facilitate creation of LC-H_N fusions through recombination.

135

DNA coding for LH_N/C as prepared in pENTRY2 for use in the Gateway site specific recombination cloning system. LH_N/C has a STOP codon and is thus in the correct format for recombination into an appropriate destination vector.

136

DNA coding for LH_N/C as prepared in pENTRY2 for use in the Gateway site specific recombination cloning system. LH_N/C has no STOP codon in order to facilitate creation of LH_N/C-ligand fusions through recombination.

137

DNA sequence of a pMTL vector modified to be a suitable destination vector in which to insert endopeptidase fragments from entry vectors. Vector constructed by insertion of Gateway vector conversion cassette reading frame A into pMAL-c2X. Expression cassette (ptac promoter, male gene, Gateway cassette and polylinker)

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subsequently cloned into pMTL.

138 DNA coding for LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion in which the LC-H_N junction incorporates a specific enterokinase protease activation site and the ligand is spaced from the H_N domain by a peptide sequence derived from an Rnase A loop

139 LH_N/A-ligand (*Erythrina cristagalli* lectin) fusion produced by expression of SEQ ID 138, in which the LC-H_N junction incorporates a specific enterokinase protease activation site and the ligand is spaced from the H_N domain by a peptide sequence derived from an Rnase A loop

140 DNA coding for tetanus toxin

141 Tetanus toxin produced by expression of SEQ ID 140, said polypeptide incorporating the LC, H_N and H_C domains

142 DNA coding for LH_N of tetanus toxin, in which the 3' end of the clone encodes the sequenceGlu-Glu-Asp-Ile-Asp-Val-STOP, terminating at residue Val879

143 LH_N of tetanus toxin produced by expression of SEQ ID 142, said polypeptide terminating with the sequenceGlu-Glu-Asp-Ile-Asp-Val-STOP, terminating at residue Val879.

144 DNA coding for LH_N of tetanus toxin, in which the 3' end of the clone encodes the sequenceGlu-Glu-Asp-Ile-Asp-Val-STOP as in SEQ ID 142. The clone also incorporates a specific enterokinase protease activation site at the junction of the LC and H_N domain...

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145 LH_N of tetanus toxin produced by expression of SEQ ID 144, said polypeptide terminating with the sequenceGlu-Glu-Asp-Ile-Asp-Val-STOP as in SEQ ID 143. The protein also incorporates a specific enterokinase protease activation site at the junction of the LC and H_N domain.

146 DNA coding for LH_N of tetanus toxin, in which the 3' end of the clone encodes the sequenceGlu-Glu-Asp-Ile-Asp-Val-Ile-Leu-Lys-Lys-Ser-Thr-Ile-Leu-STOP, terminating at residue Leu887

147 LH_N of tetanus toxin produced by expression of SEQ ID 146, said polypeptide terminating with the sequenceGlu-Glu-Asp-Ile-Asp-Val-Ile-Leu-Lys-Lys-Ser-Thr-Ile-Leu-STOP, terminating at residue Leu887

148 DNA encoding ₂LH₄₂₃/A(Q₂E)

149 ₂LH₄₂₃/A(Q₂E), which is a single polypeptide comprising a BoNT/A L-chain and the N-terminal 423 amino acid residues of a BoNT/A H-chain. The polypeptide has been generated by cleavage from a GST purification tag and has a 2 amino acid extension (GS) on the N-terminus of the L-chain resulting from the proteolytic cleavage of the L-chain from the purification tag. The polypeptide has a variant amino acid residue E at position 2 compared with Q in a native serotype A L-chain.

150 DNA encoding ₂LH₄₂₃/A(Q₂E), wherein the DNA has an *E. coli* codon bias.

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- 151 ${}^2\text{LH}_{423}/\text{A}(\text{Q}_2\text{E})$, which is equivalent to SED ID NO 149.
- 152 DNA encoding $\text{LH}_{423}/\text{A}(\text{Q}_2\text{E})$, wherein the DNA has an *E. coli* codon bias.
- 153 $\text{LH}_{423}/\text{A}(\text{Q}_2\text{E})$, which is equivalent to SEQ ID NO 151 but without any N-terminal extension to the L-chain.
- 154 DNA encoding $\text{LH}_{423}/\text{A}(\text{Q}_2\text{E})$.
- 155 $\text{LH}_{423}/\text{A}(\text{Q}_2\text{E})$, which is equivalent to SEQ ID NO 149 but without any N-terminal extension to the L-chain.
- 156 DNA encoding ${}^2\text{L}_{\text{FXa}}/{}^3\text{H}_{423}/\text{A}(\text{Q}_2\text{E})$.
- 157 ${}^2\text{L}_{\text{FXa}}/{}^3\text{H}_{423}/\text{A}(\text{Q}_2\text{E})$, which is equivalent to SEQ ID NO 151 and wherein a Factor Xa cleavage site has been introduced between the L-chain and H-chain components of the polypeptide.
- 158 DNA encoding $\text{LH}_{423}/\text{A}(\text{Q}_2\text{E})\text{-6His}$.
- 159 $\text{LH}_{423}/\text{A}(\text{Q}_2\text{E})\text{-6His}$, which is a native LH_N molecule and includes a C-terminal poly-His purification tag.
- 160 DNA encoding ${}^2\text{L}_{\text{FXa}}/{}^3\text{H}_{423}/\text{A}(\text{Q}_2\text{E})_{\text{FXa}}\text{-6His}$.
- 161 ${}^2\text{L}_{\text{FXa}}/{}^3\text{H}_{423}/\text{A}(\text{Q}_2\text{E})_{\text{FXa}}\text{-6His}$, which is equivalent to SEQ ID NO 157 and includes a Factor Xa cleavage site to facilitate removal of the poly-His purification tag.
- 162 DNA encoding ${}^2\text{LH}_{423}/\text{A}(\text{Q}_2\text{E}, \text{H}_{227}\text{Y})$.

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- 163 ${}_{2}\text{LH}_{423}/\text{A}(\text{Q}_{2}\text{E}, \text{H}_{227}\text{Y})$, which is equivalent to SEQ ID NO 149 and wherein the polypeptide has a variant amino acid residue Y at position 227 compared with H in a native serotype A L-chain.
- 164 DNA encoding ${}_{2}\text{LH}_{423}/\text{A}(\text{Q}_{2}\text{E}, \text{H}_{227}\text{Y})$, wherein the DNA has an *E. coli* codon bias.
- 165 ${}_{2}\text{LH}_{423}/\text{A}(\text{Q}_{2}\text{E}, \text{H}_{227}\text{Y})$, which is equivalent to SEQ ID NO 163.
- 166 DNA encoding ${}_{2}\text{LH}_{423}/\text{A}(\text{Q}_{2}\text{E}, \text{E}_{224}\text{Q})$, wherein the DNA has an *E. coli* codon bias.
- 167 ${}_{2}\text{LH}_{423}/\text{A}(\text{Q}_{2}\text{E}, \text{E}_{224}\text{Q})$, which is equivalent to SEQ ID NO 151 and wherein the polypeptide has a variant amino acid residue Q at position 224 compared with E in a native serotype A L-chain.
- 168 DNA encoding ${}_{2}\text{LH}_{423}/\text{A}(\text{Q}_{2}\text{E}, \text{E}_{224}\text{Q}, \text{H}_{227}\text{Y})$, wherein the DNA has an *E. coli* codon bias.
- 169 ${}_{2}\text{LH}_{423}/\text{A}(\text{Q}_{2}\text{E}, \text{E}_{224}\text{Q}, \text{H}_{227}\text{Y})$, which is equivalent to SEQ ID NO 167 and wherein the polypeptide has a variant amino acid residue Y at position 227 compared with H in a native serotype A L-chain.
- 170 DNA encoding $\text{L}_{\text{FXa}}/\text{H}_{417}/\text{B}$.
- 171 $\text{L}_{\text{FXa}}/\text{H}_{417}/\text{B}$, which is a single polypeptide comprising a BoNT/B L-chain and the N-terminal 417 amino acid

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residues of a BoNT/B H-chain, wherein a Factor Xa cleavage site exists between the L-chain and H-chain.

172 DNA encoding L_{FXa}/H₄₁₇/B.

173 L_{FXa}/H₄₁₇/B, which is a single polypeptide comprising a BoNT/B L-chain and the N-terminal 417 amino acid residues of a BoNT/B H-chain, wherein a Factor Xa cleavage site exists between the L-chain and H-chain.

174 DNA encoding L_{FXa}/H₄₁₇/B.

175 L_{FXa}/H₄₁₇/B, which is equivalent to SEQ ID NO 173, wherein a modified linker sequence exists between the L-chain and H-chain *vis-a-vis* SEQ ID NO 173.

Example 1

A 2616 base pair, double stranded gene sequence (SEQ ID NO: 1) has been assembled from a combination of synthetic, chromosomal and polymerase-chain-reaction generated DNA (Figure 2). The gene codes for a polypeptide of 871 amino acid residues corresponding to the entire light-chain (LC, 448 amino acids) and 423 residues of the amino terminus of the heavy-chain (H_C) of botulinum neurotoxin type A. This recombinant product is designated the LH₄₂₃/A fragment (SEQ ID NO: 2).

Construction of the recombinant product

The first 918 base pairs of the recombinant gene were synthesised by concatenation of short oligonucleotides to generate a coding sequence with an *E. coli* codon bias. Both DNA strands in this region were completely synthesised as short overlapping oligonucleotides which were phosphorylated, annealed and ligated to generate the full synthetic region ending with a unique *KpnI* restriction site. The remainder of the LH₄₂₃/A

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coding sequence was PCR amplified from total chromosomal DNA from *Clostridium botulinum* and annealed to the synthetic portion of the gene.

The internal PCR amplified product sequences were then deleted and replaced with the native, fully sequenced, regions from clones of *C. botulinum* chromosomal origin to generate the final gene construct. The final composition is synthetic DNA (bases 1-913), polymerase amplified DNA (bases 914-1138 and 1976-2616) and the remainder is of *C. botulinum* chromosomal origin (bases 1139-1975). The assembled gene was then fully sequenced and cloned into a variety of *E. coli* plasmid vectors for expression analysis.

Expression of the recombinant gene and recovery of protein product

The DNA is expressed in *E. coli* as a single nucleic acid transcript producing a soluble single chain polypeptide of 99,951 Daltons predicted molecular weight. The gene is currently expressed in *E. coli* as a fusion to the commercially available coding sequence of glutathione S-transferase (GST) of *Schistosoma japonicum* but any of an extensive range of recombinant gene expression vectors such as pEZZ18, pTrc99, pFLAG or the pMAL series may be equally effective as might expression in other prokaryotic or eukaryotic hosts such as the Gram positive bacilli, the yeast *P. pastoris* or in insect or mammalian cells under appropriate conditions.

Currently, *E. coli* harbouring the expression construct is grown in Luria-Bertani broth (L-broth pH 7.0, containing 10 g/l bacto-tryptone, 5 g/l bacto-yeast extract and 10 g/l sodium chloride) at 37° C until the cell density (biomass) has an optical absorbance of 0.4- 0.6 at 600 nm and the cells are in mid-logarithmic growth phase. Expression of the gene is then induced by addition of isopropylthio-β-D-galactosidase (IPTG) to a final concentration of 0.5 mM. Recombinant gene expression is allowed to proceed for 90 min at a reduced temperature of 25°C. The cells are then harvested by centrifugation, are resuspended in a buffer solution containing 10 mM Na₂HPO₄, 0.5 M NaCl, 10 mM EGTA, 0.25% Tween, pH 7.0 and then frozen at -20°C. For extraction of the recombinant protein the cells are disrupted by sonication. The cell extract is then cleared of debris by centrifugation and the cleared supernatant fluid containing soluble recombinant fusion

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protein (GST- LH₄₂₃/A) is stored at -20°C pending purification. A proportion of recombinant material is not released by the sonication procedure and this probably reflects insolubility or inclusion body formation. Currently we do not extract this material for analysis but if desired this could be readily achieved using methods known to those skilled in the art.

The recombinant GST- LH₄₂₃/A is purified by adsorption onto a commercially prepared affinity matrix of glutathione Sepharose and subsequent elution with reduced glutathione. The GST affinity purification marker is then removed by proteolytic cleavage and reabsorption to glutathione Sepharose; recombinant LH₄₂₃/A is recovered in the non-adsorbed material.

Construct variants

A variant of the molecule, LH₄₂₃/A (Q₂E,N₂₆K,A₂₇Y) (SEQ ID NO: 26) has been produced in which three amino acid residues have been modified within the light chain of LH₄₂₃/A producing a polypeptide containing a light chain sequence different to that of the published amino acid sequence of the light chain of BoNT/A .

Two further variants of the gene sequence that have been expressed and the corresponding products purified are ₂₃LH₄₂₃/A (Q₂E,N₂₆K,A₂₇Y) (SEQ ID NO: 4) which has a 23 amino acid N-terminal extension as compared to the predicted native L-chain of BoNT/A and ₂LH₄₂₃/A (Q₂E,N₂₆K,A₂₇Y) (SEQ ID NO: 6) which has a 2 amino acid N-terminal extension (Figure 4).

In yet another variant a gene has been produced which contains a *Eco* 47 III restriction site between nucleotides 1344 and 1345 of the gene sequence given in (SEQ ID NO: 1). This modification provides a restriction site at the position in the gene representing the interface of the heavy and light chains in native neurotoxin, and provides the capability to make insertions at this point using standard restriction enzyme methodologies known to those skilled in the art. It will also be obvious to those skilled in the art that any one of a number of restriction sites could be so employed, and that the *Eco* 47 III insertion simply

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exemplifies this approach. Similarly, it would be obvious for one skilled in the art that insertion of a restriction site in the manner described could be performed on any gene of the invention. The gene described, when expressed, codes for a polypeptide, L_{1/4}H₄₂₃/A (SEQ ID NO: 10), which contains an additional four amino acids between amino acids 448 and 449 of LH₄₂₃/A at a position equivalent to the amino terminus of the heavy chain of native BoNT/A.

A variant of the gene has been expressed, L_{FXa/3}H₄₂₃/A (SEQ ID NO: 12), in which a specific proteolytic cleavage site was incorporated at the carboxy-terminal end of the light chain domain, specifically after residue 448 of L_{1/4}H₄₂₃/A. The cleavage site incorporated was for Factor Xa protease and was coded for by modification of SEQ ID NO: 1. It will be apparent to one skilled in the art that a cleavage site for another specified protease could be similarly incorporated, and that any gene sequence coding for the required cleavage site could be employed. Modification of the gene sequence in this manner to code for a defined protease site could be performed on any gene of the invention.

Variants of L_{FXa/3}H₄₂₃/A have been constructed in which a third domain is present at the carboxy-terminal end of the polypeptide which incorporates a specific binding activity into the polypeptide.

Specific examples described are:

(1) L_{FXa/3}H₄₂₃/A-IGF-1 (SEQ ID NO: 14), in which the carboxy-terminal domain has a sequence equivalent to that of insulin-like growth factor-1 (IGF-1) and is able to bind to the insulin-like growth factor receptor with high affinity;

(2) L_{FXa/3}H₄₂₃/A-CtxA14 (SEQ ID NO: 16), in which the carboxy-terminal domain has a sequence equivalent to that of the 14 amino acids from the carboxy-terminus of the A-subunit of cholera toxin (CtxA) and is thereby able to interact with the cholera toxin B-subunit pentamer; and

(3) L_{FXa/3}H₄₂₃/A-ZZ (SEQ ID NO: 18), in which the carboxy-terminal domain is a tandem

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repeating synthetic IgG binding domain. This variant also exemplifies another modification applicable to the current invention, namely the inclusion in the gene of a sequence coding for a protease cleavage site located between the end of the clostridial heavy chain sequence and the sequence coding for the binding ligand. Specifically in this example a sequence is inserted at nucleotides 2650 to 2666 coding for a genenase cleavage site. Expression of this gene produces a polypeptide which has the desired protease sensitivity at the interface between the domain providing H_N function and the binding domain. Such a modification enables selective removal of the C-terminal binding domain by treatment of the polypeptide with the relevant protease.

It will be apparent that any one of a number of such binding domains could be incorporated into the polypeptide sequences of this invention and that the above examples are merely to exemplify the concept. Similarly, such binding domains can be incorporated into any of the polypeptide sequences that are the basis of this invention. Further, it should be noted that such binding domains could be incorporated at any appropriate location within the polypeptide molecules of the invention.

Further embodiments of the invention are thus illustrated by a DNA of the invention further comprising a desired restriction endonuclease site at a desired location and by a polypeptide of the invention further comprising a desired protease cleavage site at a desired location.

The restriction endonuclease site may be introduced so as to facilitate further manipulation of the DNA in manufacture of an expression vector for expressing a polypeptide of the invention; it may be introduced as a consequence of a previous step in manufacture of the DNA; it may be introduced by way of modification by insertion, substitution or deletion of a known sequence. The consequence of modification of the DNA may be that the amino acid sequence is unchanged, or may be that the amino acid sequence is changed, for example resulting in introduction of a desired protease cleavage site, either way the polypeptide retains its first and second domains having the properties required by the invention.

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Figure 10 is a diagrammatic representation of an expression product exemplifying features described in this example. Specifically, it illustrates a single polypeptide incorporating a domain equivalent to the light chain of botulinum neurotoxin type A and a domain equivalent to the H_N domain of the heavy chain of botulinum neurotoxin type A with a N-terminal extension providing an affinity purification domain, namely GST, and a C-terminal extension providing a ligand binding domain, namely an IgG binding domain. The domains of the polypeptide are spatially separated by specific protease cleavage sites enabling selective enzymatic separation of domains as exemplified in the Figure. This concept is more specifically depicted in Figure 11 where the various protease sensitivities are defined for the purpose of example.

Assay of product activity

The LC of botulinum neurotoxin type A exerts a zinc-dependent endopeptidase activity on the synaptic vesicle associated protein SNAP-25 which it cleaves in a specific manner at a single peptide bond. The ₂LH₄₂₃/A (Q₂E,N₂₆K,A₂₇Y) (SEQ ID NO: 6) cleaves a synthetic SNAP-25 substrate *in vitro* under the same conditions as the native toxin (Figure 3). Thus, the modification of the polypeptide sequence of ₂LH₄₂₃/A (Q₂E,N₂₆K,A₂₇Y) relative to the native sequence and within the minimal functional LC domains does not prevent the functional activity of the LC domains.

This activity is dependent on proteolytic modification of the recombinant GST-₂LH₄₂₃/A (Q₂E,N₂₆K,A₂₇Y) to convert the single chain polypeptide product to a disulphide linked dichain species. This is currently done using the proteolytic enzyme trypsin. The recombinant product (100-600 µg/ml) is incubated at 37°C for 10-50 minutes with trypsin (10 µg/ml) in a solution containing 140 mM NaCl, 2.7 mM KCl, 10 mM Na₂HPO₄, 1.8 mM KH₂PO₄, pH 7.3. The reaction is terminated by addition of a 100-fold molar excess of trypsin inhibitor. The activation by trypsin generates a disulphide linked dichain species as determined by polyacrylamide gel electrophoresis and immunoblotting analysis using polyclonal anti-botulinum neurotoxin type A antiserum.

₂LH₄₂₃/A is more stable in the presence of trypsin and more active in the *in vitro* peptide

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cleavage assay than is ${}_{23}\text{LH}_{423}/\text{A}$. Both variants, however, are fully functional in the *in vitro* peptide cleavage assay. This demonstrates that the recombinant molecule will tolerate N-terminal amino acid extensions and this may be expanded to other chemical or organic moieties as would be obvious to those skilled in the art.

Example 2

As a further exemplification of this invention a number of gene sequences have been assembled coding for polypeptides corresponding to the entire light-chain and varying numbers of residues from the amino terminal end of the heavy chain of botulinum neurotoxin type B. In this exemplification of the disclosure the gene sequences assembled were obtained from a combination of chromosomal and polymerase-chain-reaction generated DNA, and therefore have the nucleotide sequence of the equivalent regions of the natural genes, thus exemplifying the principle that the substance of this disclosure can be based upon natural as well as a synthetic gene sequences.

The gene sequences relating to this example were all assembled and expressed using methodologies as detailed in Sambrook J, Fritsch E F & Maniatis T (1989) Molecular Cloning: A Laboratory Manual (2nd Edition), Ford N, Nolan C, Ferguson M & Ockler M (eds), Cold Spring Harbor Laboratory Press, New York, and known to those skilled in the art.

A gene has been assembled coding for a polypeptide of 1171 amino acids corresponding to the entire light-chain (443 amino acids) and 728 residues from the amino terminus of the heavy chain of neurotoxin type B. Expression of this gene produces a polypeptide, LH_{728}/B (SEQ ID NO: 20), which lacks the specific neuronal binding activity of full length BoNT/B.

A gene has also been assembled coding for a variant polypeptide, LH_{417}/B (SEQ ID NO: 22), which possesses an amino acid sequence at its carboxy terminus equivalent by amino acid homology to that at the carboxy-terminus of the heavy chain fragment in native LH_N/A .

A gene has also been assembled coding for a variant polypeptide, LH₁₀₇/B (SEQ ID NO: 24) , which expresses at its carboxy-terminus a short sequence from the amino terminus of the heavy chain of BoNT/B sufficient to maintain solubility of the expressed polypeptide.

Construct Variants

A variant of the coding sequence for the first 274 bases of the gene shown in SEQ ID NO: 21 has been produced which whilst being a non-native nucleotide sequence still codes for the native polypeptide.

Two double stranded, a 268 base pair and a 951 base pair, gene sequences have been created using an overlapping primer PCR strategy. The nucleotide bias of these sequences was designed to have an *E.coli* codon usage bias.

For the first sequence, six oligonucleotides representing the first (5') 268 nucleotides of the native sequence for botulinum toxin type B were synthesised. For the second sequence 23 oligonucleotides representing internal sequence nucleotides 691-1641 of the native sequence for botulinum toxin type B were synthesised. The oligonucleotides ranged from 57-73 nucleotides in length. Overlapping regions, 17-20 nucleotides, were designed to give melting temperatures in the range 52-56°C. In addition, terminal restriction endonuclease sites of the synthetic products were constructed to facilitate insertion of these products into the exact corresponding region of the native sequence. The 268 bp 5' synthetic sequence has been incorporated into the gene shown in SEQ ID NO: 21 in place of the original first 268 bases (and is shown in SEQ ID NO: 27). Similarly the sequence could be inserted into other genes of the examples.

Another variant sequence equivalent to nucleotides 691 to 1641 of SEQ ID NO: 21 , and employing non-native codon usage whilst coding for a native polypeptide sequence, has been constructed using the internal synthetic sequence. This sequence (SEQ ID NO: 28) can be incorporated, alone or in combination with other variant sequences, in place of the

equivalent coding sequence in any of the genes of the example.

Example 3

An exemplification of the utility of this invention is as a non-toxic and effective immunogen. The non-toxic nature of the recombinant, single chain material was demonstrated by intraperitoneal administration in mice of GST-₂LH₄₂₃/A. The polypeptide was prepared and purified as described above. The amount of immunoreactive material in the final preparation was determined by enzyme linked immunosorbent assay (ELISA) using a monoclonal antibody (BA11) reactive against a conformation dependent epitope on the native LH_N/A. The recombinant material was serially diluted in phosphate buffered saline (PBS; NaCl 8 g/l, KCl 0.2 g/l, Na₂HPO₄ 1.15 g/l, KH₂PO₄ 0.2 g/l, pH 7.4) and 0.5 ml volumes injected into 3 groups of 4 mice such that each group of mice received 10, 5 and 1 micrograms of material respectively. Mice were observed for 4 days and no deaths were seen.

For immunisation, 20 µg of GST-₂LH₄₂₃/A in a 1.0 ml volume of water-in-oil emulsion (1:1 vol:vol) using Freund's complete (primary injections only) or Freund's incomplete adjuvant was administered into guinea pigs via two sub-cutaneous dorsal injections. Three injections at 10 day intervals were given (day 1, day 10 and day 20) and antiserum collected on day 30. The antisera were shown by ELISA to be immunoreactive against native botulinum neurotoxin type A and to its derivative LH_N/A. Antisera which were botulinum neurotoxin reactive at a dilution of 1:2000 were used for evaluation of neutralising efficacy in mice. For neutralisation assays 0.1 ml of antiserum was diluted into 2.5 ml of gelatine phosphate buffer (GPB; Na₂HPO₄ anhydrous 10 g/l, gelatin (Difco) 2 g/l, pH 6.5-6.6) containing a dilution range from 0.5 µg (5X10⁻⁶ g) to 5 picograms (5X10⁻¹² g). Aliquots of 0.5 ml were injected into mice intraperitoneally and deaths recorded over a 4 day period. The results are shown in Table 3 and Table 4. It can clearly be seen that 0.5 ml of 1:40 diluted anti- GST-₂LH₄₂₃/A antiserum can protect mice against intraperitoneal challenge with botulinum neurotoxin in the range 5 pg - 50 ng (1 - 10,000 mouse LD₅₀; 1 mouse LD₅₀ = 5 pg).

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TABLE 3. Neutralisation of botulinum neurotoxin in mice by guinea pig anti-GST-LH₄₂₃/A antiserum.

Survivors On Day	<u>Botulinum Toxin/mouse</u>						Control (no toxin)
	0.5µg	0.005µg	0.0005µg	0.5ng	0.005ng	5pg	
1	0	4	4	4	4	4	4
2	-	4	4	4	4	4	4
3	-	4	4	4	4	4	4
4	-	4	4	4	4	4	4

TABLE 4. Neutralisation of botulinum neurotoxin in mice by non-immune guinea pig antiserum.

Survivors On Day	<u>Botulinum Toxin/mouse</u>						Control (no toxin)
	0.5µg	0.005µg	0.0005µg	0.5ng	0.005ng	5pg	
1	0	0	0	0	0	2	4
2	-	-	-	-	-	0	4
3	-	-	-	-	-	-	4
4	-	-	-	-	-	-	4

Example 4 - Expression of recombinant LH₁₀₇/B in *E. coli*.

As an exemplification of the expression of a nucleic acid coding for a LH_N of a clostridial neurotoxin of a serotype other than botulinum neurotoxin type A, the nucleic acid sequence (SEQ ID NO: 23) coding for the polypeptide LH₁₀₇/B (SEQ ID NO: 24) was inserted into the commercially available plasmid pET28a (Novogen, Madison, WI, USA). The nucleic acid was expressed in *E. coli* BL21 (DE3) (New England BioLabs, Beverly, MA, USA) as a fusion protein with a N-terminal T7 fusion peptide, under IPTG induction at

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1 mM for 90 minutes at 37°C. Cultures were harvested and recombinant protein extracted as described previously for LH₄₂₃/A.

Recombinant protein was recovered and purified from bacterial paste lysates by immunoaffinity adsorption to an immobilised anti-T7 peptide monoclonal antibody using a T7 tag purification kit (New England bioLabs, Beverley, MA, USA). Purified recombinant protein was analysed by gradient (4-20%) denaturing SDS-polyacrylamide gel electrophoresis (Novex, San Diego, CA, USA) and western blotting using polyclonal anti-botulinum neurotoxin type antiserum or anti-T7 antiserum. Western blotting reagents were from Novex, immunostained proteins were visualised using the Enhanced Chemi-Luminescence system (ECL) from Amersham. The expression of an anti-T7 antibody and anti-botulinum neurotoxin type B antiserum reactive recombinant product is demonstrated in Figure 13.

The recombinant product was soluble and retained that part of the light chain responsible for endopeptidase activity.

The invention thus provides recombinant polypeptides useful inter alia as immunogens, enzyme standards and components for synthesis of molecules as described in WO-A-94/21300.

Example 5: Expression and purification of LH_NC

The LH_NC DNA fragment from the native clostridial neurotoxin gene was subcloned as a *Sall*-*Pst*I fragment into the expression vector pMal-c2x (New England Biolabs). The gene fragment and the protein product that would be produced after proteolytic processing from the MBP-fusion protein are defined in SEQ ID 129/130. Other commercially available expression systems such as pET vector (Novagen) pGEX vectors (Pharmacia) or pQE vectors (Qiagen) would also be suitable for expression of the gene fragments.

The expression clone was transferred into the host strain AD494 (Novagen)

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containing a pACYC plasmid carrying the tRNA genes for the codons ATA, AGA, and CTA (commercially available, for example, as Rosetta strains from Novagen). As these codons are rarely used in *E.coli*, but are frequent in the clostridial genes encoding neurotoxins, the inclusion of these tRNA genes significantly increases expression levels. Those familiar with the art would recognise that this effect is not limited to LH_N/C but is broadly applicable to all native clostridial LH_N fragments. Similar effects were observed in other host strains including HMS174 (Novagen) and TB1 (NEB), and a wide range of other hosts would be suitable for expression of these fragments.

Expression cultures of AD494 (pACYC tRNAs) pMalc2x LH_N/C were grown in Terrific Broth containing 35 µg/ml chloramphenicol, 100 µg/ml ampicillin, 1 µM ZnCl₂ and 0.5% (w/v) glucose with an overnight culture diluted 1:100 into fresh media and grown for approximately 3 hours at 37°C to an OD₆₀₀ of 0.6-1. The cultures were induced with 1 mM IPTG and grown at 30°C for 3-4 hours. Other expression systems used similar conditions except that the antibiotic was changed to kanamycin. Cells were lysed by either sonication in column buffer (20 mM Hepes 125 mM NaCl 1 µM ZnCl₂ pH 7.2) or suitable detergent treatment (e.g. Bugbuster reagent; Novagen) and cell debris pelleted by centrifugation. Supernatant proteins were loaded onto an amylose resin column equilibrated in column buffer and proteins eluted with a single step elution using column buffer with 10 mM maltose.

The MBP-LH_N/C construct used in this example has a factor Xa site situated between the MBP and LH_N domains and also has a factor Xa site between the L and H_N domains to allow the formation of the di-chain LH_N form. To remove the fusion tag and in this case to activate the LH_N fragment, the eluted protein from the amylose column is treated with factor Xa at a concentration of 1 unit protease activity per 50 µg purified fusion protein (as outlined by the manufacturer e.g. NEB) for approximately 20 hours at 25°C. The protein is then diluted 1:5 with 20 mM Hepes pH 7.2 and loaded onto a Q-sepharose fast flow column, the column washed and proteins eluted using a linear gradient of 25-500 mM NaCl in the 20 mM Hepes buffer. The free LH_N fragment is eluted at approximately 50 mM NaCl with uncleaved fusion protein and free MBP eluted

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at higher concentrations of NaCl.

Those familiar with the art will recognise that for alternative expression vectors such as pMal-c2g, where the site for removal of the MBP tag is genenase, two subsequent protease cleavage reactions would be required for removal of the fusion partner (genenase cleavage) and subsequent activation of the LH_N (factor Xa digestion). These cleavage reactions could be carried out simultaneously or with an intermediate ion exchange purification to remove contaminating proteins. An example of this model of purification/activation is identified below. These considerations are equally valid for native or synthetic activation sites as detailed in the sequence information and for LH_N fragments of all the serotypes.

Example 6 Expression and purification of LH_N/F

The LH_N fragment from the native BoNT/F gene was modified by PCR to incorporate *Bam*HI and *Hind*III, or other suitable sites, at the 5' and 3' ends respectively. The gene fragment was cloned into pET 28 to maintain the reading frames with the N-terminal His₆ purification tag. The expression clone was transferred to a host strain carrying the pACYC tRNA plasmid as outlined in example 5 and the DE3 lysogen carrying the T7 polymerase gene. Suitable host strains would include JM109, AD494, HMS174, TB1 TG1 or BL21 carrying the appropriate genetic elements. For example HMS174 (DE3) pACYC tRNA pET28a LH_N/F was used for expression and purification.

Expression cultures of HMS174 (DE3) pACYC tRNA pET28a LH_N/F were grown in Terrific Broth containing 35 µg/ml chloramphenicol, 35 µg/ml kanamycin, 1 µM ZnCl₂ and 0.5% (w/v) glucose to an OD₆₀₀ of 2.0 at 30°C and cultures were induced with 500 µM IPTG and grown at 25°C for 2 hours prior to harvest by centrifugation. The cells were lysed in 20 mM Hepes 500 mM NaCl pH 7.4 by sonication or detergent lysis and the soluble protein fraction loaded onto a metal chelate column (e.g. IMAC HiTrap column Amersham-Pharmacia) loaded with CuSO₄. Protein was eluted using a linear gradient of imidazole with His₆ LH_N/F eluting at between 50 and 250 mM imidazole.

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The His₆ tag was removed by treatment with thrombin essentially as described in Example 5. The released LH_N fragment was purified using ion exchange on a Q-sepharose column as described in Example 5.

Example 7 Expression and purification of LH_NTeNT

A native LH_NTeNT gene fragment was modified to replace the native linker region with an enterokinase cleavable linker as shown in SEQ ID 144/145 and to incorporate cloning sites at the 5' (*Bam*HI) and 3' ends (*Hind*III). This fragment was subcloned into pMAL c2x and expressed in HMS174 (pACYC tRNA) as described in Example 5. Initial purification on an amylose resin column, cleavage with factor Xa to remove the fusion tag and the ion exchange purification was also as described in Example 5 except that the positions of the elution peaks were reversed with the free MBP peak eluting before the peak for free LH_N.

Example 8 Expression of LH_N/C from a Gateway adapted expression vector.

The LH_NC fragment was cloned into a Gateway entry vector as a *Sall*-*Pst*I. Two version were made with a stop codon within the 3' *Pst*I site to terminate the protein at this position (LH_NC STOP; SEQ ID 123/124), or with no stop codon to allow the expression of the fragment with C-terminal fusion partners (LH_NC NS; SEQ ID 131/132). The entry vector was recombined with the destination vector to allow expression of the fragment with an N-terminal MBP tag. Recombination was according to standard protocols (Invitrogen Gateway expression manual).

Expression of the fusion protein from the strain AD494 (pACYC tRNA) pMTL-malE-GW LH_NC STOP, and its purification and was as described in Example 5. The addition of the additional N-terminal sequence made no significant change to the overall expression and purification. The final product following factor Xa cleavage was a disulfide bonded di-chain fragment as described above.

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For expression of the fragment with additional C-terminal domains the LH_NC NS entry vector was recombined with a destination vector carrying additional sequences following the attachment site and in the appropriate frame. The sequence of the DNA encoding the LH_N/C fragment flanked by *att* sites that has the properties necessary to facilitate recombination to create a full fusion is described in SEQ ID 133. For example, the destination vector pMTL-malE-GW-*att*-IGF was produced by subcloning the coding sequence for human IGF as an *Xba*I-*Hind*III fragment into the appropriate sites. Recombination of the LH_N/C NS fragment into this vector yielded pMTL-malE-GW-LH_NC-*att*-IGF.

This clone was expressed and purified as described above. Additional purification methods utilising the binding properties of the C-terminal IGF domain could also be used if desired.

Those familiar with the art will recognise that a similar approach could be used for other LH_N fragments from either BoNT/C or other serotypes. Similarly other C-terminal purification tags or ligands could be incorporated into destination vectors in the same way as for IGF above.

Example 9 Expression of LH_NTeNT from a Gateway adapted expression vector.

The LH_NTeNT *Bam*HI-*Hind*III fragment described in Example 7 was subcloned into an entry vector to maintain the appropriate reading frames. The entry vector was designed to incorporate a factor Xa site immediately adjacent to the *Bam*HI site such that cleavage resulted in a protein starting with the GlySer residues encoded by the *Bam*HI site. The entry vector was recombined with a commercially available destination vector carrying an N-terminal 6-His tag (e.g. pDEST17; Invitrogen). The resulting clone pDEST17 LH_NTeNT was expressed in the host strain HMS174 (pACYC tRNA). As described in Example 6. Purification of the fusion protein is also as described in Example 5 with the N-terminal His tag removed by factor Xa treatment, followed by subsequent removal of factor Xa on a Q-sepharose column.

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Example 10 Directed coupling of an LH_N/B fragment and a ligand via a fos/jun or Glu/Arg molecular clamp

LH_N/C clones of the type described in SEQ ID 115/116, 117/118, 119/120 & 121/122 were expressed and purified as previously indicated in Example 5. Purified, activated LH_N/C protein was then mixed with an equimolar amount of ligand tagged with the complementary clamp partner (jun-tagged ligand for SEQ ID 117/118 and 121/122; poly-arginine-tagged ligand for SEQ ID 115/116 and 119/120). Proteins were gently mixed to facilitate association, then purified to isolate associated ligand-endopeptidase fragment.

Example 11 Directed coupling of an LH_NTeNT fragment and a ligand via an acid/base molecular clamp

LH_NTeNT clones of the type described in SEQ ID 142/143, 144/145 & 146/147 were modified to incorporate one component of the acid/base leucine zipper clamping system. Following expression and purification of the tagged proteins as previously indicated in Example 5, the association with tagged ligand was performed essentially as described in Example 10.

Example 12 Activation of LH_N/B, carrying a thrombin protease processing site, to yield a di-chain fragment

As in SEQ ID 99/100 an LH_N/B carrying a thrombin site in the linker between the L and H_N domains was expressed from pMAL c2x essentially as described in Example 5. The purified LH_N/B fragment was incubated with 1 unit thrombin per mg protein for 20 hours at 25°C. The di-chain LH_N was separated from the thrombin by further purification on a Q-sepharose column as described in Example 5

Example 13 Activation of LH_NTeNT carrying an enterokinase processing site to yield a di-chain fragment

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To prepare activated di-chain LH_N the purified protein (e.g. obtained from SEQ ID 144/145) was treated with enterokinase at a concentration of 1 enzyme unit per 50 µg purified protein at 25°C for 20 hours. The activated di-chain LH_N was then purified from the enterokinase by ion exchange on a Q-sepharose column under identical conditions to that used for the purification following factor Xa cleavage (as described in Example 5) or using a benzamidine sepharose column equilibrated in 20 mM Hepes 100 mM NaCl pH 7.2 to specifically bind and remove the enterokinase.